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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 23, 2003, 16:50:56 : Search time 24.5 Seconds

(Without alignments)  
490.657 Million cell updates/sec

Title: US-09-865-321a-4\_COPY\_26\_150

Sequence: 1 AMHVAPAVYLASSRGIAF.....GIGNGTQIYVIDPEPCDSD 125

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database:

1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Query Length	DB ID	Description
1	634	96.5	223	2	cytotoxic T-lympho
2	631	96.0	186	2	cytotoxic T-lympho
3	552	84.0	223	2	CTLA-4 precursor
4	453	68.9	223	2	cytotoxic T-lympho
5	150	22.8	221	2	CD28 protein - ch
6	137	20.9	173	2	cell surface prote
7	131	19.9	221	2	CD28 precursor - r
8	130.5	19.9	220	1	T-cell surface gly
9	121	18.4	218	2	T-cell surface gly
10	114	17.4	218	2	T-cell surface gly
11	94.5	14.4	140	2	PL0013
12	93	14.2	124	2	S40336
13	92.5	14.1	120	2	S46370
14	90	13.7	125	2	S40353
15	89.5	13.6	105	2	S26338
16	89.5	13.6	132	2	S38646
17	88.5	13.5	132	2	S31603
18	87.5	13.3	128	2	S46372
19	87	13.2	104	2	JC6076
20	87	13.2	108	2	S30521
21	86.5	13.2	108	2	S36277
22	86	13.1	111	1	KVRB36
23	85.5	13.0	212	2	S70431
24	85	12.9	120	2	S30525
25	85	12.9	129	2	S40369
26	84.5	12.9	111	2	PN0537
27	84.5	12.9	117	2	S46371
28	84.5	12.9	132	2	S40334
29	84.5	12.9	213	2	A21177

30	84	12.8	112	2	PL00274	Ig kappa chain V r
31	83.5	12.7	106	2	PL0082	Ig kappa chain V r
32	83.5	12.7	107	2	S12954	Ig kappa chain V r
33	83.5	12.6	112	2	H26317	Ig kappa chain V r
34	83	12.6	107	2	S36275	Ig kappa chain V r
35	83	12.6	113	2	S30523	Ig kappa chain V r
36	83	12.6	113	2	S34003	Ig kappa chain V r
37	82.5	12.6	235	2	S14675	Ig kappa chain V r
38	82	12.5	108	2	G30560	Ig kappa chain V r
39	82	12.5	133	2	S40378	Ig kappa chain V r
40	81.5	12.4	79	2	A28840	Ig kappa chain V r
41	81.5	12.4	130	2	A32513	Ig kappa chain pre
42	81.5	12.4	197	2	S29593	Ig kappa chain (M
43	81.5	12.4	233	2	S29577	Ig kappa chain pre
44	81.5	12.4	234	2	S14237	Ig kappa chain pre
45	81	12.3	94	2	S26340	Ig light chain V r

#### ALIGNMENTS

```

RESULT 1
T09536
cytotoxic T-lymphocyte protein 4 - human
C:Species: Homo sapiens (man)
C>Date: 16-Jul-1999 #sequence-revision 16-Jul-1999 #text-change 21-Jul-2000
C:Accession: T09536
R:Harper, K.; Balzano, C.; Rouvier, E.; Mattei, M.G.; Luciani, M.F.; Golstein, P.
J. Immunol. 147, 1037-1044, 1991
A:Title: CTLA-4 and CD28 activated lymphocyte molecules are closely related in both m
A:Reference number: I49584; MUID:91318145; PMID:1713603
A:Accession: T09536
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-223 <HAR>
A:Cross-references: EMBL:LI5006; NID:g291928; PIDN:AMB59385.1; PID:g291929
C:Genetics:
A:Gene: CTLA4
A:Map position: 2q33
C:Superfamily: T-cell surface glycoprotein CD28; immunoglobulin homology
C:Keywords: T-cell; transmembrane protein

Query Match          96.5%  Score 634; DB 2; Length 223;
Best Local Similarity 97.6%  Pred. No. 1.9e-56;
Matches 122; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 AMHVAPAVYLASSRGIAFVCEYASPGKTEFRVTVLRQADSQVTEVCATYMGNELT 60
        |||||||
Db       37 AMHVAPAVYLASSRGIAFVCEYASPGKTEFRVTVLRQADSQVTEVCATYMGNELT 96
        |||||||

QY      61 FLDDICTGTSSGNQVNLITQGLRAMDTGLTYCKVELMPPPYEGINGTQIYVIDPEP 120
        |||||||
Db       97 FLDDICTGTSSGNQVNLITQGLRAMDTGLTYCKVELMPPPYEGINGTQIYVIDPEP 156
        |||||||

QY      121 CPDSD 125
        |||||||
Db       157 CPDSD 161

RESULT 2
S08614
cytotoxic T-lymphocyte protein 4 - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 07-Sep-1990 #sequence-revision 07-Sep-1990 #text-change 11-Jan-2000
C:Accession: S08614
R:Darivach, P.; Mattei, M.G.; Golstein, P.; Lefranc, M.P.
Eur. J. Immunol. 18, 1901-1905, 1988
A:Title: Human Ig superfamily CTLA-4 gene: chromosomal localization and identity of p
A:Reference number: S08614; MUID:89120925; PMID:3220103
A:Accession: S08614
A:Molecule type: DNA
A:Residues: 1-186 <DAR>
A:Cross-references: EMBL:X15070; NID:g30283; PID:g825649

```

C:Genetics:  
A:Gene: GDB:CTLA4  
A:Cross-references: GDB:119818; OMIM:123890  
A:Map position: 2q33-2q33  
A:Introns: 116/1; 152/3  
C:Superfamily: T-cell surface glycoprotein CD28; immunoglobulin homology  
C:Keywords: transmembrane protein  
F:125-150/Domain: transmembrane #status predicted <TM>  
F:151-186/Domain: intracellular #status predicted <INT>  
F:21-92/Dsulfide bonds: #status predicted

Query Match  
Best Local Similarity 97.6%; Score 631; DB 2; Length 186;  
Matches 121; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 MHVAPAVYVLASSRGISFVCEYASPGKTEVRVTVLRQADSVTEVCATYMGNELTF 61  
DB 1 MHVAPAVYVLASSRGISFVCEYASPGKTEVRVTVLRQADSVTEVCATYMGNELTF 60  
QY 62 LDDSTCTGSSGNQVNLITQGLRAMDTGLYICKVELMPPPYEGISGNGTQIYVIDPEPC 121  
DB 61 LDDSTCTGSSGNQVNLITQGLRAMDTGLYICKVELMPPPYEGISGNGTQIYVIDPEPC 120  
QY 122 PDSD 125  
DB 121 PDSD 124

## RESULT 3

14696  
CTLA-4 precursor - rabbit  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C:Date: 14-Feb-1997 #sequence\_revision 14-Feb-1997 #text\_change 05-Nov-1999  
C:Accession: I46696  
R:Isono, T.; Seto, A.  
Immunogenetics 42, 217-220, 1995  
A:Title: Cloning and sequencing of the rabbit gene encoding T-cell costimulatory molecule  
A:Reference number: I46696; MUID:95369849; PMID:7642234  
A:Accession: I46696  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-223 <ISO>  
A:Cross-references: GB:D49844; NID:9755100; PIDN:BA08644.1; PID:9755101  
C:Superfamily: T-cell surface glycoprotein CD28; immunoglobulin homology

Query Match  
Best Local Similarity 84.0%; Score 552; DB 2; Length 223;  
Matches 104; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

QY 1 AMHVAOPAVYVLASSRGISFVCEYASPGKTEVRVTVLRQADSVTEVCATYMGNELTF 60  
DB 37 ALHVSQPAVYVLASSRGISFVCEYASPGKTEVRVTVLRQADSVTEVCATYMGNELTF 96  
QY 61 FLDDSTCTGSSGNQVNLITQGLRAMDTGLYICKVELMPPPYEGISGNGTQIYVIDPEP 120  
DB 97 FLDDSTCTGSSGNQVNLITQGLRAMDTGLYICKVELMPPPYEGISGNGTQIYVIDPEP 156  
QY 121 CPDSD 125  
DB 157 CPDSD 161

## RESULT 4

A29063  
cytotoxic T-lymphocyte protein 4 - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 21-May-1988 #sequence\_revision 21-May-1988 #text\_change 05-Nov-1999  
C:Accession: A29063; I49622  
R:Bruneet, J.F.; Dentzot, F.; Luciani, M.F.; Roux-Dosseto, M.; Suzan, M.; Mattei, M.G.;  
Nature 328, 267-270, 1987  
A:Title: A new member of the immunoglobulin superfamily--CTLA-4.  
A:Reference number: A29063; MUID:87258259; PMID:3496540  
A:Accession: A29063

A:Molecule type: mRNA  
A:Residues: 1-223 <BR>  
A:Cross-references: GB:X05719; NID:950592; PIDN:CAA29191.1; PID:950593  
R:Harper, K.; Balzano, C.; Rouvier, E.; Mattei, M.G.; Luciani, M.F.; Golstein, P.  
J. Immunol. 147, 1037-1044, 1991  
A:Title: CTLA-4 and CD28 activated lymphocyte molecules are closely related in both m  
A:Reference number: I49584; MUID:91318145; PMID:1713603  
A:Accession: I49622  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-36 <RES>  
A:Cross-references: GB:M74362; NID:9192833; PIDN:AAA37489.1; PID:9553903  
C:Genetics:  
A:Gene: Ctla-4  
A:Map position: 1, band C  
C:Superfamily: T-cell surface glycoprotein CD28; immunoglobulin homology  
C:Keywords: transmembrane protein

Query Match  
Best Local Similarity 68.9%; Score 453; DB 2; Length 223;  
Matches 85; Conservative 16; Mismatches 24; Indels 0; Gaps 0;

QY 1 AMHVAOPAVYVLASSRGISFVCEYASPGKTEVRVTVLRQADSVTEVCATYMGNELTF 60  
DB 37 ALHVSQPAVYVLASSRGISFVCEYASPGKTEVRVTVLRQADSVTEVCATYMGNELTF 96  
QY 61 FLDDSTCTGSSGNQVNLITQGLRAMDTGLYICKVELMPPPYEGISGNGTQIYVIDPEP 120  
DB 97 FLDDSTCTGSSGNQVNLITQGLRAMDTGLYICKVELMPPPYEGISGNGTQIYVIDPEP 156  
QY 121 CPDSD 125  
DB 157 CPDSD 161

## RESULT 5

S25168  
CHT28 protein - chicken  
C:Species: Gallus gallus (chicken)  
C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Jul-1999  
C:Accession: I50619; S25168  
R:Young, J.R.; Davison, T.F.; Tregaskes, C.A.; Rennie, M.C.; Vainio, O.  
J. Immunol. 152, 3848-3851, 1994  
A:Title: Monomeric homologue of mammalian CD28 is expressed on chicken T cells.  
A:Reference number: I50619; MUID:94194147; PMID:8144954  
A:Accession: I50619  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-221 <Y02>  
A:Cross-references: EMBL:X67915; NID:963221; PIDN:CAA48114.1; PID:963222  
C:Superfamily: T-cell surface glycoprotein CD28; immunoglobulin homology  
C:Keywords: transmembrane protein

Query Match  
Best Local Similarity 22.8%; Score 150; DB 2; Length 221;  
Matches 40; Conservative 21; Mismatches 45; Indels 12; Gaps 5;

QY 4 VAOPAVYVLASSRGISFVCEYASPGKTEVRVTVLRQADSVTEVCATYMGNELTF 63  
DB 23 VAOPAVYVLASSRGISFVCEYASPGKTEVRVTVLRQADSVTEVCATYMGNELTF 76  
QY 64 DSI-----CTGSSGNQVNLITQGLRAMDTGLYICKVELMPPPYEGISGNGTQIYVIDPEP 115  
DB 77 SNNKREFNGRHDHDKVIFNLMMNSASOTDIYFKIEAMPPPYVYNNKSNCTIYV 134

## RESULT 6

I46197  
cell surface protein - dog (fragment)  
C:Species: Canis lupus familiaris (dog)  
C:Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 21-Jan-2000  
C:Accession: I46197  
R:Pastori, R.L.; Milde, K.F.; Alejandro, R.

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 23, 2003, 16:43:01 ; Search time 13.5 Seconds

(without alignments)  
435,432 Million cell updates/sec

Title: US-09-865-321a-4\_COPY\_26\_150  
Perfect score: 657  
Sequence: 1 AMHVAQPAVVLASSRGIASF.....GICNGRIYVIDPEPCDSD 125

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_41:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	640	97.4	223	1	CTL4_HUMAN
2	552	84.0	223	1	P16410 homo sapien
3	549	83.6	223	1	P42072 oryctolagus
4	453	68.9	223	1	09MYX7 sus scrofa
5	150	22.8	221	1	P09793 mus musculu
6	133.5	20.3	219	1	P11043 gallus galli
7	131	19.9	221	1	Q28071 bos taurus
8	130.5	19.9	220	1	P42069 oryctolagus
9	121	18.4	218	1	P10747 homo sapien
10	114	17.4	218	1	CD28_MOUSE
11	86	13.1	111	1	CD28_RAT
12	81	12.3	129	1	P11693 oryctolagus
13	80.5	12.3	108	1	P1824 homo sapien
14	80	12.2	108	1	P01599 homo sapien
15	79.5	12.1	111	1	VCA1_RAT
16	79	12.0	111	1	P29534 rattus norv
17	79	12.0	111	1	P01709 homo sapien
18	78	11.9	111	1	P01707 homo sapien
19	77.5	11.8	108	1	Q96R16 xanthomomas
20	77.5	11.8	108	1	Q96R16 homo sapien
21	77.5	11.8	108	1	P01689 oryctolagus
22	77.5	11.7	111	1	P01600 homo sapien
23	76.5	11.6	108	1	P01631 mus musculu
24	76.5	11.6	108	1	P01704 homo sapien
25	76	11.6	109	1	P04945 mus musculu
26	76	11.6	109	1	P01633 mus musculu
27	75.5	11.5	114	1	P01624 homo sapien
28	75.5	11.5	113	1	P01625 homo sapien
29	75.5	11.5	113	1	P01668 oryctolagus
30	75	11.4	3707	1	P01668 mus musculu
31	75	11.4	366	1	Q05793 mus musculu
32	74.5	11.3	1356	1	P01810 mus musculu
33	74.5	11.3	109	1	P35968 homo sapien
			109	1	P01681 rattus norv
			1	1	P01708 homo sapien

34	74.5	11.3	113	1	KV2F_MOUSE	P01630 mus musculu
35	74.5	11.3	436	1	HSLU_RHILIO	Q96CUI rhizobium 1
36	74	11.3	480	1	SAHH_XYLEFA	Q9PEJ1 xyfella fas
37	74	11.3	715	1	LCCL_LACIA	Q9CJL8 lactococcus
38	73.5	11.2	111	1	LY2C_HUMAN	P01706 homo sapien
39	73.5	11.2	136	1	HY01_XENLA	P20956 xenopus lae
40	73.5	11.2	136	1	KV5B_MOUSE	P01634 mus musculu
41	73.5	11.2	466	1	SAHH_BRONE	Q9YE49 bruceella me
42	73	11.1	106	1	LV4B_HUMAN	P01716 homo sapien
43	73	11.1	112	1	KV2D_MOUSE	P01629 mus musculu
44	73	11.1	112	1	LV6B_HUMAN	P01722 homo sapien
45	73	11.1	119	1	HY3M_HUMAN	P01774 homo sapien

## ALIGNMENTS

RESULT 1

ID	CTLA4_HUMAN	STANDARD	PRT	223 AA.
AC	P16410; Q8WXJ1; Q96P43; Q9UKN9;			
DT	01-AUG-1990 (Rel. 15, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Cytotoxic T-lymphocyte protein 4 precursor (Cytotoxic T-lymphocyte-associated antigen 4) (CTLA-4) (CD152 antigen).			
GN	CTLA4 OR CD152.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
CC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
NC	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	MEDLINE-21601151; PubMed-11735222;			
RT	Ling V., Wu P.W., Finnerty H.F., Agostino M.J., Graham J.R., Chen S.,			
RT	Jussif J., Fisk G.J., Miller C.P., Collins M.,			
RT	"Assembly and annotation of human chromosome 2q33 sequence containing			
RT	the CD28, CTLA4, and ICOS gene cluster: analysis by computational,			
RT	comparative, and microarray approaches."			
RL	Genomics 78:155-168(2001).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	Wu P.W., Ling V.,			
RT	"Full length sequence of hCTLA4 cDNA."			
RT	Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.			
RL	[3]			
RP	SEQUENCE OF 1-37 FROM N.A.			
RA	MEDLINE-91318145; PubMed-1713603;			
RT	Harper K., Balzano C., Rouvier E., Mattei M.-G., Luciani M.F.,			
RT	Golstein P.,			
RT	"CTLA-4 and CD28 activated lymphocyte molecules are closely related			
RT	in both mouse and human as to sequence, message expression, gene			
RT	structure, and chromosomal location."			
RL	J. Immunol. 147:1037-1044(1991).			
RN	[4]			
RP	SEQUENCE OF 38-223 FROM N.A.			
RA	TISSUE-Lymphocytes;			
RT	MEDLINE-99120925; PubMed-3220103;			
RT	Darivach P., Mattei M.-G., Golstein P., Lefranc M.-P.,			
RT	"Human Ig superfamily CTLA-4 gene: chromosomal localization and			
RT	identity of protein sequence between murine and human CTLA-4			
RT	cytoplasmic domains."			
RL	Eur. J. Immunol. 18:1901-1905(1988).			
RN	[5]			
RP	SEQUENCE OF 140-223 FROM N.A., AND TISSUE SPECIFICITY.			
RA	MEDLINE-99425274; PubMed-10493833;			
RT	Ling V., Wu P.W., Finnerty H.F., Sharpe A.H., Gray G.S., Collins M.,			
RT	"Complete sequence determination of the mouse and human CTLA4 gene			
RT	loci: cross-species DNA sequence similarity beyond exon borders."			
RL	Genomics 60:341-355(1999).			
RN	[6]			
RP	FUNCTION.			
RA	MEDLINE-91341416; PubMed-1714933;			

RA Linsley P.S., Brady W., Unnes M., Grismaire L.S., Damlé N.K.,  
 RA Ledbetter J.A.:  
 RT "CTLA-4 is a second receptor for the B cell activation antigen B7.";  
 RL J. Exp. Med. 174:361-369(1991).  
 RN [7]  
 RN STRUCTURE BY NMR OF P7-165.  
 RP MEDLINE-97372869; PubMed-9228944;  
 RX Metzler W.J., Bajorath J., Fenderson W., Shaw S.Y., Constantine K.L.,  
 RA Nemura P.S., Leytze G., Peach R.J., Layole T.B., Mueller L.,  
 RA Linsley P.S.:  
 RT "Solution structure of human CTLA-4 and delineation of a CD80/CD86  
 RT binding site conserved in CD28.";  
 RL Nat. Struct. Biol. 4:527-531(1997).  
 RN [8]  
 RN VARIANT ALA-17, AND ASSOCIATION WITH IDDM12.  
 RP MEDLINE-97402209; PubMed-9259273;  
 RX Marron M.P., Raffel L.J., Garchon H.-J., Jacob C.O., Serrano-Rios M.,  
 RA Martinez Larrad M.T., Teng W.-P., Park Y., Zhang Z.-X.,  
 RA Goldstein D.R., Tao Y.-W., Beaurain G., Bach J.-F., Huang H.-S.,  
 RA Luo D.-F., Zeldner A., Rotter J.I., Yang M.C.K., Modilevsky T.,  
 RA MacLaren N.K., She J.-X.:  
 RT "Insulin-dependent diabetes mellitus (IDDM) is associated with CTLA4  
 RT polymorphisms in multiple ethnic groups.";  
 RL Hum. Mol. Genet. 6:1275-1282(1997).  
 RN [9]  
 RN POLYMORPHISM, AND ASSOCIATION WITH COELIAC DISEASE.  
 RP MEDLINE-99205840; PubMed-10189842;  
 RX Djilali-Saah I., Schmitz J., Harfouch-Hamoud E., Mougnot J.-F.,  
 RA Bach J.-F., Caillat-Zucman S.:  
 RT "CTLA-4 gene polymorphism is associated with predisposition to coeliac  
 RT disease.";  
 RL Gut 43:167-169(1996).  
 RN [10]  
 RN VARIANT ALA-17, AND ASSOCIATION WITH TAO.  
 RP MEDLINE-99402177; PubMed-10475192;  
 RX Valdivia B., Imlrie H., Perros P., Dickinson J., McCarthy M.I.,  
 RA Kendall-Taylor P., Pearce S.H.S.:  
 RT "Cytotoxic T lymphocyte antigen-4 (CTLA-4) gene polymorphism confers  
 RT susceptibility to thyroid associated orbitopathy.";  
 RL Lancet 354:743-744(1999).  
 RN [11]  
 RN VARIANT ALA-17, AND ASSOCIATION WITH GRD.  
 RP MEDLINE-20385252; PubMed-10924276;  
 RX Chistyakov D.A., Savost'yanov K.V., Turakulov R.I., Petulina N.A.,  
 RA Trukhina L.V., Kudnova A.V., Balabolkin M.I., Nosikov V.V.:  
 RT "Complex association analysis of Graves disease using a set of  
 RT polymorphic markers.";  
 RL Mol. Genet. Metab. 70:214-218(2000).  
 RN [12]  
 RN VARIANT ALA-17.  
 RP MEDLINE-20395844; PubMed-10903931;  
 RX Deng Z., Morse J.H., Slager S.L., Cierzo N., Moore K.J., Vaneetos G.,  
 RA Kalachikov S., Cayanis E., Fischer S.G., Barst R.O., Hodge S.E.,  
 RA Knowles J.A.:  
 RT "Familial primary pulmonary hypertension (gene PPH1) is caused by  
 RT mutations in the bone morphogenetic protein receptor-II gene.";  
 RL Am. J. Hum. Genet. 67:737-744(2000).  
 RN [13]  
 RN FUNCTION. POSSIBLY INVOLVED IN T-CELL ACTIVATION. BINDS TO B7-1  
 CC (CD80) AND B7-2 (CD86).  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- TISSUE SPECIFICITY: Widely expressed with highest levels in  
 CC lymphoid tissues.  
 CC -1- POLYMORPHISM: The variant Ala-17 is associated with an increased  
 CC risk for autoimmune disorders as Graves disease (GRD), type I  
 CC insulin-dependent diabetes mellitus (IDDM12), and thyroid-  
 CC associated orbitopathy (TAO). The variant Thr-17 is associated  
 CC with predisposition to coeliac disease, a gluten sensitive  
 CC enteropathy characterized by small bowel mucosal atrophy.  
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.  
 CC -1- DATABASE: NAME=PROV; NOTE=CD guide CD152 entry;  
 CC WWW=http://www.ncbi.nlm.nih.gov/prov/cd/cd152.htm".

```

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CC on the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.ebi.ac.uk/announcements
CC or send an email to license@ebi.ac.uk.)
CC
DR EMBL; AF411058; AAL0932.1; -.
DR EMBL; AF414120; AAL07473.1; -.
DR EMBL; M74363; AAA52127.1; -.
DR EMBL; M37243; AAA52773.1; JOINED.
DR EMBL; M37244; AAA52773.1; JOINED.
DR EMBL; AF142144; AAF02499.1; -.
DR PIR; S08614; S08614.
DR PDB; 1AH1; 15-APR-98.
DR PDB; 1HE6; 28-NOV-01.
DR PDB; 1I85; 04-APR-01.
DR PDB; 1I8L; 04-APR-01.
DR Genew; HGNC:12505; CTLL4.
DR MIM; 123890; -.
DR GO; GO:0005887; C:Integral to plasma membrane; TAS.
DR GO; GO:0006955; P:Immune response; TAS.
DR InterPro; IPR003596; Ig_V.
DR SMART; SM00409; Ig; 1.
DR SMART; SM00406; Ig; 1.
DR PROSITE; PSS0835; IG-LIKE; FALSE_NEG.
KW Immunoglobulin domain; T-cell; Transmembrane; Glycoprotein; Signal;
KW 3D-structure; Polymorphism.
FT SIGNAL 1 35
FT CHAIN 36 223 POTENTIAL.
FT DOMAIN 36 161 CYTOTOXIC T-LYMPHOCYTE PROTEIN 4.
FT TRANSMEM 162 187 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 188 223 POTENTIAL.
FT DISULFID 39 140 CYTOPLASMIC (POTENTIAL).
FT DISULFID 58 129 IG-LIKE V-TYPE.
FT CARBOHYD 85 103
FT VARIANT 113 113
FT VARIANT 17 17
FT CONFLICT 147 147 N-LINKED (GLCNAC... ) (POTENTIAL).
FT STRAND 45 47 T->A (In dbSNP:231775).
FT TURN 50 51 /FTID-VAR_013577.
FT STRAND 53 59 T->A (in REF. 4).
FT STRAND 70 76
FT STRAND 81 86
FT TURN 91 92
FT TURN 99 100
FT STRAND 104 108
FT TURN 109 110
FT STRAND 111 117
FT TURN 121 123
FT STRAND 125 132
FT TURN 137 138
FT STRAND 142 143
FT STRAND 147 150
SO SEQUENCE 223 AA; 24656 MW; 6P9466FB2E139A5A CRC64;

Query Match 97.4%; Score 640; DB 1; Length 223;
Best Local Similarity 96.4%; Pred. No. 6.5e-59;
Matches 123; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AMHAQAQAVVLIASRGSIASFVCEYASPGKYTEVAVVILROADSOVTEVCATYMMGNELT 60
Db AMHAQAQAVVLIASRGSIASFVCEYASPGKATEVAVVILROADSOVTEVCATYMMGNELT 96
QY FLDDSICTGTSSGNQVNLTTIOLGRAMDYGLYICKVELMTPPPYEGIGNGTQIVIDPEP 120
Db FLDDSICTGTSSGNQVNLTTIOLGRAMDYGLYICKVELMTPPPYVYLGIGNGTQIVIDPEP 156
QY 121 CPDSD 125
Db 157 CPDSD 161

```

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 23, 2003, 16:50:26 ; Search time 60 Seconds

(Without alignments)  
537.610 Million cell updates/sec

Title: US-09-865-321a-4\_COPY\_26\_150

Perfect score: 657

Sequence: 1 AMHYAQAQPAVAVLASSRGIAASF.....GIGNGTQIYVIDPPECPSD 125

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 segs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_23:\*

1: sp\_archaea:\*

2: sp\_bacteria:\*

3: sp\_fungi:\*

4: sp\_human:\*

5: sp\_invertebrate:\*

6: sp\_mammal:\*

7: sp\_mhc:\*

8: sp\_organelle:\*

9: sp\_phage:\*

10: sp\_plant:\*

11: sp\_rodent:\*

12: sp\_virus:\*

13: sp\_vertebrate:\*

14: sp\_unclassified:\*

15: sp\_virus:\*

16: sp\_bacteriopl:\*

17: sp\_archaeop:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	638	97.1	223	6	Q9BD4 macaca mla
2	638	97.1	223	6	Q9BD7 papio anubi
3	634	96.5	160	4	Q8TDA6 homo sapien
4	595	90.6	223	6	Q9BDP1 actus trivi
5	584	88.9	137	4	Q95653 homo sapien
6	579	88.1	115	4	Q9BZK2 homo sapien
7	564	85.8	223	6	Q9T02 canis fami
8	564	85.8	223	6	Q9GKP2 canis fami
9	561	85.4	223	11	Q9JLV3 marmota mon
10	560	85.2	223	6	Q9XTA1 felis silve
11	560	85.2	223	6	Q9XSY7 felis silve
12	550	83.7	223	6	Q9XST1 felis silve
13	549	83.6	223	6	Q9N186 sus scrofa
14	543	82.6	221	6	Q28090 bos taurus
15	530	80.7	221	6	Q97631 ovis aries
16	475	72.3	223	11	Q62859 ratius norv

17	420	63.9	174	11	Q9Z1A7	Q9Z1A7 ratius norv
18	252	36.4	68	11	Q9PEP8	Q9PEP8 cricetus
19	180	27.4	102	11	Q8CH94	Q8CH94 mus musculus
20	142	21.6	221	11	Q9JLV4	Q9JLV4 marmota mon
21	137	20.9	173	6	Q28289	Q28289 canis fami
22	137	20.9	221	6	Q9N088	Q9N088 canis fami
23	137	20.9	221	6	Q9GKP3	Q9GKP3 canis fami
24	133.5	20.3	219	6	Q97630	Q97630 ovis aries
25	133	20.2	221	6	Q02757	Q02757 felis silve
26	132	20.1	221	6	Q9N214	Q9N214 felis silve
27	130.5	19.9	220	6	Q9BDM6	Q9BDM6 macaca neme
28	129.5	19.7	138	6	Q8HYR9	Q8HYR9 bos taurus
29	129.5	19.7	220	6	Q9BDN5	Q9BDN5 cercopithec
30	128	19.5	220	6	Q9BDN2	Q9BDN2 callithrix
31	126.5	19.3	220	6	Q9BDN8	Q9BDN8 papio anubi
32	125.5	19.1	220	6	Q9BDM6	Q9BDM6 macaca mla
33	121	18.4	218	11	Q8CPB3	Q8CPB3 mus musculu
34	110	16.7	44	11	Q9Z1A8	Q9Z1A8 mus musculu
35	96	14.6	192	11	Q8CG11	Q8CG11 ratius norv
36	96	14.6	192	11	Q8CFD9	Q8CFD9 ratius norv
37	95	14.5	108	4	Q9UL79	Q9UL79 homo sapien
38	91.5	13.9	176	6	Q95JH8	Q95JH8 macaca fasc
39	91.5	13.9	180	6	Q8MJ02	Q8MJ02 macaca mla
40	90.5	13.8	51	6	Q8MIS6	Q8MIS6 bos taurus
41	90.5	13.8	235	11	Q91W12	Q91W12 mus musculu
42	88.5	13.5	177	4	Q14930	Q14930 homo sapien
43	88.5	13.5	190	4	Q14932	Q14932 homo sapien
44	88.5	13.5	201	4	Q14931	Q14931 homo sapien
45	86	13.1	151	6	Q8MJ01	Q8MJ01 macaca mla

## ALIGNMENTS

RESULT 1	ID	Q9BD4	PRELIMINARY	PRT	223 AA
AC	Q9BD4	01-JUN-2001 (TREMBLrel. 17, Created)			
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)				
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)				
DE	CD152 protein precursor.				
CN	CTRA-4				
OS	Macaca mulatta (Rhesus macaque),				
OS	Macaca nemestrina (Pig-tailed macaque), and				
OS	Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).				
CC	Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;				
CC	Mammalia: Eutheria: Primates: Catarrhini: Cercopitheidae;				
CC	Cercopitheidae; Macaca.				
OX	NCBI_TaxID=9544, 9545, 9531;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	SPECIES=M.mulatta, M.nemestrina, and C.torquatus atys;				
RA	Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,				
RA	Weiss W.R., Ansari A.A.;				
RT	"Cloning, sequencing and homology analysis of nonhuman primate				
RT	Ins/Ras ligand and co-stimulatory molecules.";				
RL	Immunogenetics 0:0-0(2001).				
DR	EMBL: AF344846; AKR37605.1; -				
DR	EMBL: AF344854; AKR37537.1; -				
DR	EMBL: AF344848; AKR37608.1; -				
DR	HSSP: P16410; IAH1.				
DR	InterPro: IPR003596; Ig_V.				
DR	SMART: SMO0406; IGV; I.				
KW	SIGNAL.				
FT	SIGNAL.				
FT	VARIANT	1	37	POTENTIAL.	
FT	SEQUENCE	223	223	N->D.	
SO	SEQUENCE	223	223	MM; BDE42248A00398FA CRC64;	
Query Match 97.1%; Score 638; DB 6; Length 223;					
Best Local Similarity 97.6%; Pred. No. 8.7e-61;					
Matches 122; Conservative 1; Mismatches 2; Indels 0; Gaps 0;					

QY 1 AMHVAPAVVLASSRGISFVCEYASPGKTEVRVTVLRQADSOVTEVCAATYMMGNELT 60  
 DB 37 AMHVAPAVVLASSRGISFVCEYASPGKATEVRVTVLRQADSOVTEVCAATYMMGNELT 96  
 QY 61 FLDDSICTGTSSGNQVNLTIQGLRAMDTGLYICKVELMPPPYEGISGNGTOIYIDPEP 120  
 DB 97 FLDDSICTGTSSGNQVNLTIQGLRAMDTGLYICKVELMPPPYMGISGNGTOIYIDPEP 156  
 QY 121 CPDSD 125  
 DB 157 CPDSD 161

## RESULT 2

Q9BDN7 PRELIMINARY; PRT; 223 AA.

AC Q9BDN7; 01-JUN-2001 (TREMblrel. 17, Created)  
 DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)  
 DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)  
 DE CD152 protein precursor.  
 GN CTLA-4.  
 OS Papio anubis (Olive baboon).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;  
 OC Cercopitheciinae; Papio.  
 OX NCBI\_TaxID=9555;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-21383618; PubMed-11491535;  
 RA Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,  
 RA Weiss W.R., Ansari A.A.;  
 RT "Cloning, sequencing, and homology analysis of nonhuman primate  
 RT Fas/Fas-1 ligand and co-stimulatory molecules."  
 RL EMBL; AF344838; AAK37534.1; -  
 RL EMBL; AF344838; AAK37534.1; -  
 DR HSSP; P16410; IAH1.  
 DR InterPro: IPR003596; Ig-V.  
 DR SMART; SM00406; IGV; 1.  
 KW Signal.  
 FT SIGNAL.  
 SQ SEQUENCE 223 AA; 24655 MW; EC18C279CC65668 CRC64;

Query Match 97.1%; Score 638; DB 6; Length 223;  
 Best Local Similarity 97.6%; Pred. No. 8,7e-61;  
 Matches 122; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 AMHVAPAVVLASSRGISFVCEYASPGKTEVRVTVLRQADSOVTEVCAATYMMGNELT 60  
 DB 37 AMHVAPAVVLASSRGISFVCEYASPGKATEVRVTVLRQADSOVTEVCAATYMMGNELT 96  
 QY 61 FLDDSICTGTSSGNQVNLTIQGLRAMDTGLYICKVELMPPPYEGISGNGTOIYIDPEP 120  
 DB 97 FLDDSICTGTSSGNQVNLTIQGLRAMDTGLYICKVELMPPPYMGISGNGTOIYIDPEP 156  
 QY 121 CPDSD 125  
 DB 157 CPDSD 161

## RESULT 3

Q8TDA6 PRELIMINARY; PRT; 160 AA.

AC Q8TDA6; 01-JUN-2002 (TREMblrel. 21, Created)  
 DT 01-JUN-2002 (TREMblrel. 21, Last sequence update)  
 DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)  
 DE CT1A4 (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiinae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RA Guo J.H., Fan M.W., Bian Z., Jia R.;  
 RT "Partial sequence of CT1A4 mRNA, signal peptide and extracellular  
 RT domain."  
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF486806; AAL9664.1; -  
 DR InterPro: IPR003596; Ig-V.  
 DR SMART; SM00406; IGV; 1.  
 FT NON\_TER 160  
 SQ SEQUENCE 160 AA; 17470 MW; 1385B4644F63836F CRC64;

Query Match 96.5%; Score 634; DB 4; Length 160;  
 Best Local Similarity 98.4%; Pred. No. 1.5e-60;  
 Matches 122; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AMHVAPAVVLASSRGISFVCEYASPGKTEVRVTVLRQADSOVTEVCAATYMMGNELT 60  
 DB 37 AMHVAPAVVLASSRGISFVCEYASPGKATEVRVTVLRQADSOVTEVCAATYMMGNELT 96  
 QY 61 FLDDSICTGTSSGNQVNLTIQGLRAMDTGLYICKVELMPPPYEGISGNGTOIYIDPEP 120  
 DB 97 FLDDSICTGTSSGNQVNLTIQGLRAMDTGLYICKVELMPPPYMGISGNGTOIYIDPEP 156  
 QY 121 CPDSD 124  
 DB 157 CPDSD 160

## RESULT 4

Q9BDP1 PRELIMINARY; PRT; 223 AA.

AC Q9BDP1; 01-JUN-2001 (TREMblrel. 17, Created)  
 DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)  
 DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)  
 DE CD152 protein precursor.  
 GN CTLA-4.  
 OS Aotus trivirgatus (Night monkey) (Douroucoulli).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.  
 OX NCBI\_TaxID=9505;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-21383618; PubMed-11491535;  
 RA Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,  
 RA Weiss W.R., Ansari A.A.;  
 RT "Cloning, sequencing, and homology analysis of nonhuman primate  
 RT Fas/Fas-1 ligand and co-stimulatory molecules."  
 RL EMBL; AF344834; AAK37530.1; -  
 RL EMBL; AF344834; AAK37530.1; -  
 DR HSSP; P16410; IAH1.  
 DR InterPro: IPR003599; Ig.  
 DR SMART; SM00409; IGV; 1.  
 KW Signal.  
 FT SIGNAL.  
 SQ SEQUENCE 223 AA; 24813 MW; 3F702052117C1431 CRC64;

Query Match 90.6%; Score 595; DB 6; Length 223;  
 Best Local Similarity 90.4%; Pred. No. 3.8e-56;  
 Matches 113; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 AMHVAPAVVLASSRGISFVCEYASPGKTEVRVTVLRQADSOVTEVCAATYMMGNELT 60  
 DB 37 AMHVAPAVVLASSRGISFVCEYASPGKATEVRVTVLRQADSOVTEVCAATYMMGNELT 96  
 QY 61 FLDDSICTGTSSGNQVNLTIQGLRAMDTGLYICKVELMPPPYEGISGNGTOIYIDPEP 120  
 DB 97 FLDDSICTGTSSGNQVNLTIQGLRAMDTGLYICKVELMPPPYMGISGNGTOIYIDPEP 156  
 QY 121 CPDSD 125  
 DB 157 CPDSD 161

GenCore version 5.1.6.  
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OM protein - protein search, using sw model

Run on: August 23, 2003, 16:43:01 ; Search time 60.5 Seconds  
(without alignments)  
327.947 Million cell updates/sec

Title: US-09-865-321A-4\_COPY\_26\_150

Sequence: 1 AMHVAPAVVLASSRGIAF.....GICNGIOIYIDPEPCDSD 125

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

1: /Geneseq\_19Jun03: \*  
2: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1980.DAT: \*  
3: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1981.DAT: \*  
4: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1982.DAT: \*  
5: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1983.DAT: \*  
6: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1984.DAT: \*  
7: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1985.DAT: \*  
8: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1986.DAT: \*  
9: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1987.DAT: \*  
10: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1988.DAT: \*  
11: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1989.DAT: \*  
12: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1990.DAT: \*  
13: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1991.DAT: \*  
14: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1992.DAT: \*  
15: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1993.DAT: \*  
16: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1994.DAT: \*  
17: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1995.DAT: \*  
18: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1996.DAT: \*  
19: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1997.DAT: \*  
20: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1998.DAT: \*  
21: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2000.DAT: \*  
22: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2001.DAT: \*  
23: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2002.DAT: \*  
24: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2003.DAT: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	657	100.0	383	23	ABB78102
2	657	100.0	383	23	AAAM50654
3	657	100.0	383	23	AAU75120
4	657	100.0	383	23	AAAB47862
5	657	100.0	383	24	ABP56717
6	652	99.2	383	23	ABB78105
7	652	99.2	383	23	AAU75123
8	652	99.2	383	24	ABP56721
9	649	98.8	212	23	AAU75127

10	649	98.8	212	23	AAU75132	Human CTLA4 recept
11	649	98.8	383	23	ABB78103	Amino acid sequenc
12	649	98.8	383	23	AAU75121	Human soluble CTLA
13	649	98.8	383	24	ABP56719	CTLA4 mutant L104E
14	648	98.6	212	23	AAU75131	Human CTLA4 recept
15	648	98.6	383	23	ABB78101	Amino acid sequenc
16	648	98.6	383	23	ABB78104	Amino acid sequenc
17	648	98.6	383	23	AAAM50655	Soluble CTLA4 muta
18	648	98.6	383	23	AAU75119	Human soluble CTLA
19	648	98.6	383	23	AAU75122	Human soluble CTLA
20	648	98.6	383	24	ABP56718	CTLA4 mutant L104E
21	648	98.6	383	24	ABP56720	CTLA4 mutant L104E
22	644	98.0	212	23	AAU75129	Human CTLA4 recept
23	643	97.9	212	23	AAU75130	Human CTLA4 recept
24	642	97.7	212	23	AAU75126	Human CTLA4 recept
25	641	97.6	212	23	AAU75128	Human CTLA4 recept
26	640	97.4	187	20	AAV41130	CTLA4 receptor wit
27	640	97.4	187	20	AAW97615	Human CTLA recepto
28	640	97.4	187	20	AAW97610	Human CTLA recepto
29	640	97.4	211	20	AAW97560	Human CTLA4 recept
30	640	97.4	212	15	AAW31040	Human CTLA4 recept
31	640	97.4	212	15	AAW60134	CTLA4 receptor fus
32	640	97.4	212	16	AAW76642	Full length CTLA4
33	640	97.4	212	20	AAW43479	Amino acid sequenc
34	640	97.4	212	20	AAW81584	Human CTLA4 recept
35	640	97.4	212	23	ABB78106	Amino acid sequenc
36	640	97.4	212	23	AAU75124	Human CTLA4 recept
37	640	97.4	212	24	ABP56715	Human CTLA4 recept
38	640	97.4	223	21	AAV15129	Human CTLA-4 prote
39	640	97.4	223	23	AAU74508	Human cytotoxic T-
40	640	97.4	223	23	AAU74509	Human cytotoxic T-
41	640	97.4	364	21	AAW93658	Fusion protein of
42	640	97.4	374	18	AAW26206	CTLA4-1964 fusion
43	640	97.4	374	18	AAW26207	CTLA4-modified IgG
44	640	97.4	377	18	AAW26208	CTLA4-modified IgG
45	640	97.4	383	23	ABB78107	Amino acid sequenc

#### ALIGNMENTS

RESULT 1  
ABB78102  
ID ABB78102 standard; Protein: 383 AA.  
XX  
AC ABB78102;  
XX  
DT 05-NOV-2002 (first entry)  
XX  
DE Amino acid sequence of a CTLA4Ig mutant, designated L104EA29YIg.  
XX  
KW CTLA4Ig; mutant; L104EA29YIg; CTLA4; immunoglobulin; Ig; B7;  
KW immunosuppressive; mixed haematopoietic chimerism; transplanted tissue;  
KW T cell depleted bone marrow cell; T cell costimulatory signal;  
KW haemoglobinopathy; beta-thalassemia; sickle cell disease;  
KW organ rejection.  
XX  
OS Synthetic.  
XX  
PN WO200258729-A2.  
XX  
PD 01-AUG-2002.  
XX  
PE 25-JAN-2002; 2002WO-0503780.  
XX  
PR 26-JAN-2001; 2001US-264528P.  
XX  
PR 05-JUL-2001; 2001US-303142P.  
XX  
PA (UYEM-) UNIV EMORY.  
XX  
PI Larsen CP, Pearson TC, Waller EK, Adams AB;  
XX  
DR WPI, 2002-619143/66.



XX Establishing mixed hematopoietic chimerism in subject after  
PT transplantation, by administering T cell depleted bone marrow cells,  
PT alkylating agent, immunosuppressive composition that blocks T cell  
PT costimulatory signals -  
PS Example 8; Fig 15; 16pp; English.  
XX  
XX The present sequence represents a CTLA4lg mutant, designated L104EA29Ylg.  
CC CTLA4lg is a soluble fusion protein, comprising an extracellular domain  
CC of wild type CTLA4 joined to an immunoglobulin (Ig) tail or a portion  
CC thereof which binds a B7 molecule. The present protein has the mutations  
CC A29Y and L104E. CTLA4lg and its mutants are examples of immunosuppressive  
CC agents that may be used in the method of the invention. The specification  
CC describes a method of establishing mixed hematopoietic chimerism in  
CC a subject with a transplanted tissue. The method comprises administering  
CC to the subject, T cell depleted bone marrow cells, an alkylating agent  
CC and an immunosuppressive composition that blocks T cell costimulatory  
CC signals in the subject, thus establishing hematopoietic chimerism in the  
CC subject. The method is useful for treating hematopoietic chimerism in the  
CC (e.g. beta-thalassemia or sickle cell disease), in a subject by  
CC establishing hematopoietic chimerism. It is also useful for inhibiting  
CC rejection of an organ or tissue transplanted into the subject.  
XX  
SQ Sequence 383 AA:  
Query Match 100.0%; Score 657; DB 23; Length 383;  
Best Local Similarity 100.0%; Pred. No. 1.8e-58;  
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AMHVAQPAVAVLASSRGIAFVCEYASPGKTEYEVTVLRQADSOVTEVCAATYMGNELT 60  
DB 26 AMHVAQPAVAVLASSRGIAFVCEYASPGKTEYEVTVLRQADSOVTEVCAATYMGNELT 85  
QY 61 FLDDSTCTGTSSGNOVNLITGCRAMDGTGTYCKVELMPPPYEGIGNTQIYVIDPEP 120  
DB 86 FLDDSTCTGTSSGNOVNLITGCRAMDGTGTYCKVELMPPPYEGIGNTQIYVIDPEP 145  
QY 121 CPDSD 125  
DB 146 CPDSD 150  
RESULT 2  
AAM50654  
AAM50654 standard; Protein; 383 AA.  
AC AAM50654;  
XX  
XX 04-APR-2002 (first entry)  
XX  
DE Soluble CTLA4 mutant L104EA29Ylg.  
XX  
XX CTLA4; cytotoxic T-lymphocyte associated antigen-4; L104EA29Ylg;  
KW graft versus host disease; psoriasis; diabetes; immunosuppressive;  
KW antitumorid; antiproliferative; thymic; antitumorid;  
KW antitumorid; dermatological; antitumorid; antitumorid;  
KW neoplastic; neuroprotective; ophthalmological; antitumorid;  
KW antitumorid; antiproliferative; antitumorid; therapy; human; antibody;  
KW immunoglobulin; mutant; mutin.  
XX  
XX Homo sapiens.  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..26  
FT Protein /label= signal\_peptide  
FT Protein 27..383  
FT Protein /label= Mature\_protein  
FT Region 27..150  
FT Region /label= CTLA4  
FT Region 152..383  
FT Region /label= Immunoglobulin

XX  
PN WO200192337-A2.  
XX  
XX 06-DEC-2001.  
XX  
PD  
XX  
XX 23-MAY-2001; 2001WO-US17139.  
XX  
XX 26-MAY-2000; 2000US-0579927.  
XX  
XX 26-JUN-2000; 2000US-214065P.  
XX  
XX (BRIM ) BRISTOL-MYERS SQUIBB CO.  
XX  
XX Peach RJ, Naemura JR, Linsley PS, Bajorath J;  
DR MPI: 2002-130525/17.  
XX N-PSDB; AAI71098.  
XX  
XX Novel mutant cytotoxic T-lymphocyte-associated antigen-4 molecule which  
PT binds CD80 and/or CD86 with greater avidity than wild-type molecule, is  
PT useful for inhibiting graft versus host disease, psoriasis and diabetes  
PT  
XX  
XX Claim 6; Fig 7; 64pp; English.  
XX  
XX The present sequence is that of a novel, soluble cytotoxic  
CC T-lymphocyte-associated antigen-4 (CTLA4) mutant, designated  
CC L104EA29Ylg, in which amino acids 1-124 of the mature protein  
CC comprise the CTLA4 extracellular portion and amino acids 126-357  
CC comprise the immunoglobulin portion. The amino acid sequence of  
CC L104EA29Ylg can begin with alanine at amino acid position -1 or  
CC methionine at position +1, and ends with lysine at position +357.  
CC Compared with non-mutated CTLA4lg, L104EA29Ylg has tyrosine  
CC replacing alanine at position +29 instead of alanine, and glutamic  
CC acid replacing leucine at position +101. Mutations were introduced  
CC into CTLA4lg DNA by PCR primer-directed mutagenesis. A single  
CC mutant was initially generated, and used as template to generate  
CC the double mutant. Host-vector systems are claimed where the host  
CC is especially a COS or CHO cell. L104EA29Ylg binds approximately  
CC 2-fold more avidly than wild-type CTLA4lg to CD80 and approximately  
CC 4-fold more avidly to CD86, making it more effective than CTLA4lg at  
CC blocking immune responses. L104EA29Ylg is a claimed example of novel,  
CC soluble CTLA4 mutant molecules of the invention that recognise and  
CC bind CD80 and/or CD86. These are useful for inhibiting interaction  
CC between the CTLA4-positive T-cells and CD80 and CD86 positive cells.  
CC They are also useful for treating immune system diseases mediated by  
CC T-cell interactions with CD80 and/or CD86 positive cells by  
CC regulating T-cell interactions with the CD80 and/or CD86 positive  
CC cells. When used with a ligand reactive with interleukin-4, they  
CC are useful for inhibiting graft versus host disease (all claimed).  
CC The mutant soluble CTLA4 molecules are also useful for downregulating  
CC immune responses by inhibiting the functions of activated T-cells,  
CC such as a T-lymphocyte proliferation and cytokine secretion by  
CC suppressing T-cell responses or by inducing specific tolerance in  
CC T-cells or both, for treating immune system diseases mediated by  
CC CD28- and/or CTLA4-positive cell interactions, such as autoimmune  
CC diseases (lupus, Hashimoto's thyroiditis, primary myxedema, Grave's  
CC disease, pernicious anaemia, diabetes, Goodpasture's syndrome,  
CC Crohn's disease, multiple sclerosis, autoimmune uveitis, rheumatoid  
CC arthritis, scleroderma, etc.), immunoproliferative diseases  
CC (psoriasis, T-cell lymphoma, T-cell acute lymphoblastic leukaemia,  
CC etc.), and graft related disorders (graft versus host disease,  
CC immune disorders associated with graft transplantation rejection,  
CC chronic rejection, etc.), for inhibiting solid organ and/or tissue  
CC transplant rejection, and for treating autoimmune disorders by  
CC preventing activation of autoreactive T-cells.  
XX  
XX  
SQ Sequence 383 AA:  
Query Match 100.0%; Score 657; DB 23; Length 383;  
Best Local Similarity 100.0%; Pred. No. 1.8e-58;  
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AMHVAQPAVAVLASSRGIAFVCEYASPGKTEYEVTVLRQADSOVTEVCAATYMGNELT 60

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DB 26 AMHVAOPAVVLASSRGIAFPCEYASPKYTEVRVTYLRQDSQVTEVCATYMMGNELT 85
OY 61 FLDDSGTGTSSGNQVNLITIGLRAMDGLTYCKVELMPPPYEGINGTQIYVIDEP 120
DB 86 FLDDSGTGTSSGNQVNLITIGLRAMDGLTYCKVELMPPPYEGINGTQIYVIDEP 145
OY 121 CPDSD 125
DB 146 CPDSD 150

RESULT 3
AAU75120
ID AAU75120 standard; Protein: 383 AA.
XX
AC AAU75120;
XX
DT 09-APR-2002 (first entry)
XX
DE Human soluble CTLA4 mutant protein, L104EA29Yig.
XX
KW Human; rheumatic disease; soluble cytotoxic T lymphocyte antigen 4; Ig;
KW CTLA4; variable (V)-like extracellular domain; CTLA4ig; B7 molecule;
KW immunoglobulin constant domain; rheumatoid arthritis; autoimmune disease;
KW immune system disorder; graft-related disease; immunosuppressive; mutant;
KW immunoproliferative disease; antiinflammatory; mutant; L104EA29Yig.
XX
OS Homo sapiens.
OS Synthetic.
FH Key Location/Qualifiers
FT Peptide 1..26
FT Protein /label= Signal_peptide
FT Msc-difference 55 /label= Mature_L104EA29Yig-mutant
FT Msc-difference 130 /note= "Substitution of wild type Ala to Tyr"
FT Msc-difference 130 /note= "Substitution of wild type Leu to Glu"
XX
PN WO200202638-A2.
XX 10-JAN-2002.
XX 02-JUL-2001; 2001WO-US21204.
XX 03-JUL-2000; 2000US-215913P.
XX (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX Cohen R, Carr S, Hagerly D, Peach RJ, Becker J;
XX WPI, 2002-148002/19.
XX N-PSDB; AAS20942.
XX
XX Composition useful for treating rheumatic disease and immune system
XX disorders e.g. diabetes mellitus, graft-related disease, good pasture's
XX syndrome, comprises soluble cytotoxic T lymphocyte A4 mutant molecule
XX
XX Claim 9; Fig 19; 128pp; English.
XX
XX The present invention relates to pharmaceutical compositions and
XX methods for treating rheumatic disease. The composition comprises a
XX soluble cytotoxic T lymphocyte antigen 4 (CTLA4) mutant molecule that
XX blocks endogenous B7 molecules from binding their ligands. Soluble
XX CTLA4 molecules are constructed by fusing variable (V)-like
XX extracellular domains of CTLA4 to immunoglobulin (Ig) constant domains
XX resulting in CTLA4ig. The composition is useful for treating rheumatic
XX disease especially rheumatoid arthritis, and for alleviating a symptom
XX associated with a rheumatic disease from joint swelling, pain,
XX tenderness, and structural damage. The composition can optionally be used

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CC which other pharmaceutical agents for treating immune system disorders
CC include autoimmune diseases (e.g. systemic lupus erythematosus,
CC Addison's disease, diabetes mellitus, multiple sclerosis, Crohn's
CC disease, ulcerative colitis, Sjogren's syndrome, scleroderma and
CC sympathetic ophthalmia), graft-related diseases (e.g. graft-versus-host
CC disease), immunoproliferative diseases (e.g. psoriasis, T cell lymphoma,
CC Hashimoto's thyroiditis, pernicious anaemia and good pasture's syndrome).
CC The present sequence represents human soluble CTLA4 mutant protein,
CC L104EA29Yig.
XX
SQ Sequence 383 AA;
XX
OY Query Match 100.0%; Score 657; DB 23; Length 383;
OY Best Local Similarity 100.0%; Pred. No. 1.8e-58;
OY Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 26 AMHVAOPAVVLASSRGIAFPCEYASPKYTEVRVTYLRQDSQVTEVCATYMMGNELT 85
OY 61 FLDDSGTGTSSGNQVNLITIGLRAMDGLTYCKVELMPPPYEGINGTQIYVIDEP 120
DB 86 FLDDSGTGTSSGNQVNLITIGLRAMDGLTYCKVELMPPPYEGINGTQIYVIDEP 145
OY 121 CPDSD 125
DB 146 CPDSD 150

RESULT 4
AAB47862
ID AAB47862 standard; Protein: 383 AA.
XX
AC AAB47862;
XX
DT 15-APR-2002 (first entry)
XX
DE Human L104EA29Yig.
XX
KW Human; soluble; CTLA4; CTLA4ig; L104EA29Yig; pharmaceutical; CD28; ape;
KW B7; CD40; CD154; adhesion molecule; LFA-1; ICAM-2; ICAM-3; dog;
KW alpha-actinin; filamin; cytohesin-1; immune system; myasthenia gravis;
KW graft-versus host disease; psoriasis; graft transplant rejection; rat;
KW testicular angiocentric T cell lymphoma; benign lymphocytic angitis;
KW lupus; lupus erythematosus; lupus nephritis; Hashimoto's thyroiditis;
KW primary myxedema; Graves' disease; pernicious anaemia; Crohn's disease;
KW autoimmune atrophic gastritis; Addison's disease; diabetes; pemphigus;
KW insulin dependent diabetes mellitus; type I diabetes mellitus; rabbit;
KW good pasture's syndrome; T cell acute lymphoblastic leukemia; cat; cow;
KW sympathetic ophthalmia; autoimmune uveitis; multiple sclerosis; mouse;
KW autoimmune haemolytic anaemia; idiopathic thrombocytopenia; scleroderma;
KW primary biliary cirrhosis; chronic action hepatitis; ulcerative colitis;
KW Sjogren's syndrome; rheumatoid arthritis; polymyositis; T cell lymphoma;
KW human; monkey; horse.
XX
OS Homo sapiens.
FH Key Location/Qualifiers
FT Peptide 1..26
FT Protein /label= Oncostatin_signal_peptide
FT Msc-difference 27..383 /label= L104EA29Yig
XX
XX WO200195928-A2.
XX 20-DEC-2001.
XX
XX 08-JUN-2001; 2001WO-US18619.
XX 09-JUN-2000; 2000US-210671P.
XX (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX

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RESULT 6  
 ID ABB78105 standard; Protein: 383 AA.  
 XX ABB78105;  
 DT 05-NOV-2002 (first entry)  
 XX  
 DE Amino acid sequence of a CTLA4lg mutant, designated L104EA29Wlg.  
 XX  
 KW CTLA4lg; mutant; L104EA29Wlg; CTLA4; immunoglobulin; Ig; B7;  
 KW immunosuppressive; mixed haematopoietic chimerism; transplanted tissue;  
 KW T cell depleted bone marrow cell; T cell costimulatory signal;  
 KW haemoglobinopathy; beta-thalassemia; sickle cell disease;  
 KW organ rejection.  
 XX  
 OS Synthetic.  
 PN W0200258729-A2.  
 XX  
 PD 01-AUG-2002.  
 XX  
 PF 25-JAN-2002; 2002WO-US03780.  
 XX  
 PR 26-JAN-2001; 2001US-264528P.  
 XX  
 PR 05-JUL-2001; 2001US-303142P.  
 XX  
 PA (UYEM-) UNIV EMORY.  
 XX  
 PI Larsen CP, Pearson TC, Waller EK, Adams AB;  
 XX  
 DR WPI; 2002-619143/66.  
 DR N-PSDB; ABQ78360.  
 XX  
 PT Establishing mixed haematopoietic chimerism in subject after  
 PT transplantation, by administering T cell depleted bone marrow cells,  
 PT alkylating agent, immunosuppressive composition that blocks T cell  
 PT costimulatory signals -  
 XX  
 PS Example 8; Fig 18; 161pp; English.  
 XX  
 CC The present sequence represents a CTLA4lg mutant, designated L104EA29Wlg.  
 CC CTLA4lg is a soluble fusion protein, comprising an extracellular domain  
 CC of wild type CTLA4 joined to an immunoglobulin (Ig) tail or a portion  
 CC thereof which binds a B7 molecule. The present protein has the mutations  
 CC A29W and L104E. CTLA4lg and its mutants are examples of immunosuppressive  
 CC agents that may be used in the method of the invention. The specification  
 CC describes a method of establishing mixed haematopoietic chimerism in  
 CC a subject with a transplanted tissue. The method comprises administering  
 CC to the subject, T cell depleted bone marrow cells, an alkylating agent  
 CC and an immunosuppressive composition that blocks T cell costimulatory  
 CC signals in the subject, thus establishing haematopoietic chimerism in the  
 CC subject. The method is useful for treating haemoglobinopathy  
 CC (e.g. beta-thalassemia or sickle cell disease), in a subject by  
 CC establishing haematopoietic chimerism. It is also useful for inhibiting  
 CC rejection of an organ or tissue transplanted into the subject.  
 CC  
 SQ Sequence 383 AA;  
 XX  
 Query Match 99.2%; Score 652; DB 23; Length 383;  
 Best Local Similarity 99.2%; Pred. No. 5.8e-58;  
 Matches 124; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AMHVAQPAVYVLAASRGIAISFVCEYASPGKTEFVRYVROADSOVTEVCATYMMGNLIT 60  
 DB 26 AMHVAQPAVYVLAASRGIAISFVCEYASPGKTEFVRYVROADSOVTEVCATYMMGNLIT 85  
 QY 61 FLDDSGCTGSSGNQVNLITIGLRAMDGLYICVVELMPPPYEGIGNGTQIYIDEP 120  
 DB 86 FLDDSGCTGSSGNQVNLITIGLRAMDGLYICVVELMPPPYEGIGNGTQIYIDEP 145

QY 121 CPDSD 125  
 DB 146 CPDSD 150  
 RESULT 7  
 ID AAU75123 standard; Protein: 383 AA.  
 XX AAU75123;  
 DT 09-APR-2002 (first entry)  
 XX  
 DE Human soluble CTLA4 mutant protein, L104EA29Wlg.  
 XX  
 KW Human; rheumatic disease; soluble cytotoxic T lymphocyte antigen 4; Ig;  
 KW CTLA4; variable (V)-like extracellular domain; CTLA4lg; B7 molecule;  
 KW immunoglobulin constant domain; rheumatoid arthritis; autoimmune disease;  
 KW immune system disorder; graft-related disease; immunosuppressive; mutant;  
 KW immunoproliferative disease; antiinflammatory; mutant; L104EA29Wlg.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 EH Key Location/Qualifiers  
 FT Peptide 1..26  
 FT Protein /label= Signal\_peptide  
 FT /label= Mature\_L104EA29Wlg-mutant  
 FT Msc-difference 55  
 FT /note= "Substitution of wild type Ala to Trp"  
 FT Msc-difference 130  
 FT /note= "Substitution of wild type Leu to Glu"  
 XX  
 PN W0200202638-A2.  
 XX  
 PD 10-JAN-2002.  
 XX  
 PF 02-JUL-2001; 2001WO-US21204.  
 XX  
 PR 03-JUL-2000; 2000US-215913P.  
 XX  
 PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
 XX  
 PI Cohen R, Carr S, Hagerly D, Peach RJ, Becker J;  
 XX  
 DR WPI; 2002-148002/19.  
 DR N-PSDB; AAS20945.  
 XX  
 PT Composition useful for treating rheumatic disease and immune system  
 PT disorders e.g. diabetes mellitus, graft-related disease, good pasture's  
 PT syndrome, comprises soluble cytotoxic T lymphocyte A4 mutant molecule  
 XX  
 PS Claim 9; Fig 22; 128pp; English.  
 XX  
 CC The present invention relates to pharmaceutical compositions and  
 CC methods for treating rheumatic disease. The composition comprises a  
 CC soluble cytotoxic T lymphocyte antigen 4 (CTLA4) mutant molecule that  
 CC blocks endogenous B7 molecules from binding their ligands. Soluble  
 CC CTLA4 molecules are constructed by fusing variable (V)-like  
 CC extracellular domains of CTLA4 to immunoglobulin (Ig) constant domains  
 CC resulting in CTLA4lg. The composition is useful for treating rheumatic  
 CC disease especially rheumatoid arthritis, and for alleviating a symptom  
 CC associated with a rheumatic disease from joint swelling, pain,  
 CC tenderness, and structural damage. The composition can optionally be used  
 CC with other pharmaceutical agents for treating immune system disorders  
 CC which include autoimmune diseases (e.g. systemic lupus erythematosus,  
 CC Addison's disease, diabetes mellitus, multiple sclerosis, Crohn's  
 CC disease, ulcerative colitis, Sjogren's syndrome, scleroderma and  
 CC sympathetic ophthalmia), graft-related diseases (e.g. graft-versus-host  
 CC disease), immunoproliferative diseases (e.g. psoriasis, T cell lymphoma,  
 CC Hashimoto's thyroiditis, pernicious anaemia and good pasture's syndrome).

CC The present sequence represents human soluble CTLA4 mutant protein,  
 CC L104EA29W1g.

XX Sequence 383 AA;

Query Match 99.2%; Score 652; DB 23; Length 383;  
 Best Local Similarity 99.2%; Pred. No. 5.8e-58;  
 Matches 124; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMHVAQPAVYVLAASRGIAFVCEASPGKTEVRVYVLRQADSOVTEVCATYMGNELT 60  
 |||||  
 DB 26 AMHVAQPAVYVLAASRGIAFVCEASPGKTEVRVYVLRQADSOVTEVCATYMGNELT 85  
 |||||  
 QY 61 FLDDSTCTGSSGNQVNLITQGLRAMDTGLYICKVELMPPPYEGIGNGTOIVIDPEP 120  
 |||||  
 DB 86 FLDDSTCTGSSGNQVNLITQGLRAMDTGLYICKVELMPPPYEGIGNGTOIVIDPEP 145

QY 121 CPDSD 125  
 |||||  
 DB 146 CPDSD 150

RESULT 8  
 ABP56721  
 ID ABP56721 standard; Protein: 383 AA.

AC ABP56721;

DT 27-MAR-2003 (first entry)

XX CTLA4 mutant L104EA29W1g protein SEQ ID NO:14.

XX CTLA4; mutant; islet cell transplantation rejection inhibition;  
 KW cytotoxic T lymphocyte associated antigen-4; antidiabetic; antithyroid;  
 KW immunoprotective; neutropenic; dermatological; antipsoriatic;  
 KW diabetes; immune system disease; psoriasis; Graves' disease;  
 KW multiple sclerosis; oncostatin.  
 XX Homo sapiens.  
 OS Synthetic.

FT Key Location/Qualifiers  
 FT Peptide 1..26  
 FT Protein /label= oncostatin\_signal\_peptide  
 FT 27..383  
 FT /label= CTLA4\_mutant\_L104EA29W1g

XX W0200294202-A2.

XX 28-NOV-2002.

XX 23-MAY-2002; 2002WO-US16708.

XX 23-MAY-2001; 2001US-293402P.

XX (UYEM-) UNIV EMORY.

XX Larsen CP, Pearson TC, Adams AB;

XX WPI; 2003-140318/13.

XX N-PSDB; ABZ22588.

XX Inhibiting islet cell transplant rejection in a subject, useful for  
 PT treating diabetes by administering a cytotoxic T lymphocyte associated  
 PT antigen-4 mutant molecule

XX Claim 2; Fig 20; 100pp; English.

XX The present invention describes a method of inhibiting islet cell  
 CC transplantation rejection in a subject comprising administering a  
 CC cytotoxic T lymphocyte associated antigen-4 (CTLA-4) mutant (soluble)  
 CC molecule (I), where the subject is transplanted with islet cells before,  
 CC or after administration of (I). (I) has antidiabetic, immunoprotective,

CC neuroprotective, dermatological, antipsoriatic and antithyroid  
 CC activities. (I) can be used for inhibiting islet cell transplant  
 CC rejection in a subject e.g. a human, non-human primate (preferably  
 CC monkey), rabbit, sheep, rat, dog, cat, pig or mouse. The method is useful  
 CC for treating diabetes. (I) is also useful for treating immune system  
 CC diseases e.g. psoriasis, Graves' disease and multiple sclerosis. The  
 CC method provides a novel calcineurin inhibitor/steroid-free  
 CC immunosuppressive regimen that provides significant protection from  
 CC rejection and prolongs the survival of islet allografts in nonhuman  
 CC primates. The agent L104EA29W1g is a potent immunosuppressant, and so  
 CC replaces tacrolimus in the Edmonton protocol, thereby eliminating the  
 CC unwanted side effects of the calcineurin inhibitor. The present sequence  
 CC represents a CTLA4 mutant L104EA29W1g protein, which is used in an  
 CC example from the present invention.

QY Sequence 383 AA;  
 Query Match 99.2%; Score 652; DB 24; Length 383;  
 Best Local Similarity 99.2%; Pred. No. 5.8e-58;  
 Matches 124; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMHVAQPAVYVLAASRGIAFVCEASPGKTEVRVYVLRQADSOVTEVCATYMGNELT 60  
 |||||  
 DB 26 AMHVAQPAVYVLAASRGIAFVCEASPGKTEVRVYVLRQADSOVTEVCATYMGNELT 85  
 |||||  
 QY 61 FLDDSTCTGSSGNQVNLITQGLRAMDTGLYICKVELMPPPYEGIGNGTOIVIDPEP 120  
 |||||  
 DB 86 FLDDSTCTGSSGNQVNLITQGLRAMDTGLYICKVELMPPPYEGIGNGTOIVIDPEP 145

QY 121 CPDSD 125  
 |||||  
 DB 146 CPDSD 150

RESULT 9  
 AAV75127  
 ID AAV75127 standard; Protein: 212 AA.

AC AAV75127;

DT 09-APR-2002 (first entry)

XX Human CTLA4 receptor mutant #2.

XX Human; rheumatic disease; soluble cytotoxic T lymphocyte antigen 4; Ig;  
 KW CTLA4; variable (V)-like extracellular domain; CTLA4lg; B7 molecule;  
 KW immunoglobulin constant domain; rheumatoid arthritis; autoimmune disease;  
 KW immune system disorder; graft-related disease; immunosuppressive; mutant;  
 KW immunoproliferative disease; antiinflammatory; mutein; receptor;  
 KW oncostatin M.

XX Homo sapiens.  
 OS Synthetic.

FT Key Location/Qualifiers  
 FT Peptide 1..26  
 FT /label= Oncostatin\_M\_Signal\_peptide  
 FT Protein 27..212  
 FT /label= Mature\_CTLA4\_receptor  
 FT MISC-difference 55  
 FT /note= "Substitution of wild type Ala to any amino acid"  
 FT MISC-difference 130  
 FT /note= "Substitution of wild type Leu to Glu"

XX W0200202638-A2.

XX 10-JAN-2002.

XX 02-JUL-2001; 2001WO-US21204.

XX 03-JUL-2000; 2000US-215913P.

XX (BRIM ) BRISTOL-MYERS SQUIBB CO.



	AA	ABB78103.			
Df	XX	05-NOV-2002 .(first entry)			
Xx	XX	Amino acid sequence of a CTLA4lg mutant, designated LI04EA29LIg.			
Xx	XX				
DE	KW	CTLA4lg; mutant; LI04EA29LIg; CTLA4; immunoglobulin; Ig; B7;			
Xx	KM	immunosuppressive; mixed haematopoietic chimerism; transplanted tissue;			
Kw	KW	T cell depleted bone marrow cell; T cell costimulatory signal;			
Km	KM	haemoglobinopathy; beta-thalassemia; sickle cell disease;			
xX	xx	organ rejection.			
OS	XX	Synthetic.			
Pd	NN	WO200258729-A2.			
PD	PN	01-AUG-2002.			
pD	PP	25-JAN-2002; 2002MO-USO3780.			
XX	XX				
PR	PR	26-JAN-2001; 2001US-2645ZBP.			
Pr	PR	05-JUL-2001; 2001US-303142P.			
PA	PA	(UYEM-) UNITV EMORY.			
PI	PS	Larsen CP, Pearson TC, Waller EK, Adams AB;			
DR	DR	WPI; 2002-619143/66.			
N-	XS	N-PDSB; ABO78358.			
PT	XT	Establishing mixed haematopoietic chimerism in subject after			
pt	XP	transplantation, by administering T cell depleted bone marrow cells,			
PT	XP	alkylating agent, immunosuppressive composition that blocks T cell			
		costimulatory signals -			
		Example 8; Fig 16; 16ipp; English.			
CC	CC	The present sequence represents a CTLA4lg mutant, designated LI04EA29LIg			
CC	CC	CTLA4g is a soluble fusion protein, comprising an extracellular domain			
CC	CC	of wild type CTLA4 joined to an immunoglobulin (Ig) tail or a portion			
CC	CC	thereof which binds a B7 molecule. The present protein has the mutations			
CC	CC	A29L and L104E. CTLA4lg and its mutants are examples of immunosuppressive			
CC	CC	agents that may be used in the method of the invention. The specification			
CC	CC	describes a method of establishing mixed haematopoietic chimerism in			
CC	CC	a subject with a transplanted tissue. The method comprises administering			
CC	CC	to the subject, T cell depleted bone marrow cells, an alkylating agent			
CC	CC	and an immunosuppressive composition that blocks T cell costimulatory			
CC	CC	signals in the subject, thus establishing haematopoietic chimerism in the			
CC	CC	subject. The method is useful for treating haemoglobinopathy			
CC	CC	(e.g. beta-thalassaemia or sickle cell disease). In a subject by			
CC	CC	establishing haematopoietic chimerism. It is also useful for inhibiting			
CC	CC	rejection of an organ or tissue transplanted into the subject.			
XX	XX				
Sequence	SSQ	383 AA:			
Query Match	98.8%; Score 649; DB 23; Length 383;				
Best Local Similarity	99.2%; Pred No. 1.2e-57;				
Matches 124; Conservative 0; Mismatches 1; Indels 0; Gaps 0					
Db	I AMHVAOPAVYVLASSRGIASFVECEYSAPKRYTEVRVTVALROADSQYTEVCATFMMGNELT 60       				
Oy	I 61 FLDDSICTGTSSNONVNLTIGLRAMDRTLLTYICKLELMTPPYBYGIGNQTIVIDPEP 120       				
DB	I 86 FLDDSICTGTSSNGNVNLTIGLRAMDTGLTYICKLEVMTMPPTYEGIGNQTIVIDPEP 145       				
Oy	I 121 CPGSD 125 				
db	I 146 CPDSD 150				

XX	RESULT 12
XX	AAU75121
XX	AAU75121 standard; Protein: 383 AA.
XX	AAU75121:
XX	09-APR-2002 (first entry)
XX	Human soluble CTLA4 mutant protein, L104EA29LIg.
XX	Human: rheumatic disease; soluble cytotoxic T lymphocyte antigen 4; Ig;
XX	CTLA4; variable (V)-like extracellular domain; CTLA4lg; B7 molecule;
XX	immunoglobulin constant domain; rheumatoid arthritis; autoimmune disease;
XX	immune system disorder; graft-related disease; immunosuppressive; mteuin;
XX	immunoproliferative disease; antiinflammatory; mutant; L104EA29LIg.
XX	
OS	Homo sapiens.
OS	Synthetic.
XX	
XX	Key
XX	Location/Qualifiers
XX	1..26
XX	/label= Signal_peptide
XX	27..383
XX	/label= Mature_L104EA29LIg_mutant
XX	Misc-difference 55
XX	/note= "Substitution of wild type Ala to Leu"
XX	Misc-difference 130
XX	/note= "Substitution of wild type Leu to Glu"
XX	
XX	WO200202638-A2.
XX	
XX	10-JAN-2002.
XX	
XX	02-JUL-2001; 2001MO-US21204.
XX	
XX	03-JUL-2000; 2000US-215913P.
XX	
XX	(BRIM ) BRISTOL-MYERS SQUIBB CO.
XX	
XX	Cohen R, Carr S, Hagerly D, Peach RJ, Becker J;
XX	
XX	WPI: 2002-148002/19.
XX	N-PSDB; AAS20943.
XX	
XX	Composition useful for treating rheumatic disease and immune system
XX	disorders e.g. diabetes mellitus, graft-related disease, good pasture's
XX	syndrome, comprises soluble cytotoxic T lymphocyte A4 mutant molecule
XX	
XX	Claim 9; Fig 20; 128pp; En28pp; English.
XX	
XX	The present invention relates to pharmaceutical compositions and
XX	methods for treating rheumatic disease. The composition comprises a
XX	soluble cytotoxic T lymphocyte antigen 4 (CTLA4) mutant molecule that
XX	blocks endogenous B7 molecules from binding their ligands. Soluble
XX	CTLA4 molecules are constructed by fusing variable (V)-like
XX	extracellular domains of CTLA4 to immunoglobulin (Ig) constant domains
XX	resulting in CTLA4lg. The composition is useful for treating rheumatic
XX	disease especially rheumatoid arthritis, and for alleviating a symptom
XX	associated with a rheumatic disease from joint swelling, pain,
XX	tenderness, and structural damage. The composition can optionally be used
XX	with other pharmaceutical agents for treating immune system disorders
XX	which include autoimmune diseases (e.g. systemic lupus erythematosus,
XX	Addison's disease, diabetes mellitus, multiple sclerosis, Crohn's
XX	disease, ulcerative colitis, Sjogren's syndrome, scleroderma and
XX	sympathetic ophthalmia), graft-related diseases (e.g. graft-versus-host
XX	disease), immunoproliferative diseases (e.g. psoriasis, T cell lymphoma,
XX	Hashimoto's thyroiditis, pernicious anaemia and good pasture's syndrome),
XX	The present sequence represents human soluble CTLA4 mutant protein,
XX	L104EA29LIg.
XX	
XX	Sequence 383 AA:



Query Match 98.8%; Score 649; DB 23; Length 383;  
 Best Local Similarity 99.2%; Pred. No. 1,2e-57;  
 Matches 124; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AMHVAOPAVYVLASSRGIAFVCEYASPGKTEVRVTVLRQADSQVTEVCATYMGNELT 60  
 DB 26 AMHVAOPAVYVLASSRGIAFVCEYASPGKTEVRVTVLRQADSQVTEVCATYMGNELT 85  
 QY 61 FLDDSICTGTSSGNQVNLTIQGLRAMDTGLYICKVELMPPPYEGIGNGTQIYVIDPEP 120  
 DB 86 FLDDSICTGTSSGNQVNLTIQGLRAMDTGLYICKVELMPPPYEGIGNGTQIYVIDPEP 145

QY 121 CPDSD 125  
 DB 146 CPDSD 150

RESULT 13  
 ABP56719 standard; Protein; 383 AA.

XX AC ABP56719;  
 XX 27-MAR-2003 (first entry)  
 XX CT1A4 mutant.L104EA29LIg protein SEQ ID NO:10.  
 XX CT1A4 mutant; islet cell transplantation rejection inhibition;  
 KM cytotoxic T lymphocyte associated antigen-4; antidiabetic; antithyroid;  
 KM immunoprotective; neuroprotective; dermatological; antipsoriatic;  
 KM diabetes; immune system disease; psoriasis; Graves' disease;  
 KM multiple sclerosis; oncostatin.  
 XX Homo sapiens.  
 OS Synthetic.

XX FH Key Location/Qualifiers  
 FT Peptide 1..26  
 FT Protein /label= oncostatin\_signal\_peptide  
 FT 27..383  
 FT /label= CT1A4\_mutant.L104EA29LIg  
 PN WO200294202-A2.  
 PD 28-NOV-2002.  
 PF 23-MAY-2002; 2002WO-US16708.  
 XX 23-MAY-2001; 2001US-293402P.  
 XX (UYEM-) UNIV EMORY.  
 PA Larsen CP, Pearson TC, Adams AB;  
 XX WPI; 2003-140318/13.  
 DR N-PSDB; AB222586.  
 XX Inhibiting islet cell transplant rejection in a subject, useful for  
 PT treating diabetes by administering a cytotoxic T lymphocyte associated  
 PT antigen-4 mutant molecule  
 XX Claim 2; Fig 20; 100pp; English.

XX The present invention describes a method of inhibiting islet cell  
 CC transplantation rejection in a subject comprising administering a  
 CC cytotoxic T lymphocyte associated antigen-4 (CTLA-4) mutant (soluble)  
 CC molecule (I), where the subject is transplanted with islet cells before,  
 CC or after administration of (I). (I) has antidiabetic, immunoprotective,  
 CC neuroprotective, dermatological, antipsoriatic and antithyroid  
 CC activities. (I) can be used for inhibiting islet cell transplant  
 CC rejection in a subject e.g. a human, non-human primate (preferably  
 CC monkey), rabbit, sheep, rat, dog, cat, pig or mouse. The method is useful  
 CC for treating diabetes. (I) is also useful for treating immune system

CC diseases e.g. psoriasis, Graves' disease and multiple sclerosis. The  
 CC method provides a novel calcineurin inhibitor/steroid-free  
 CC immunosuppressive regimen that provides significant protection from  
 CC rejection and prolongs the survival of islet allografts in nonhuman  
 CC primates. The agent L104EA29LIg is a potent immunosuppressant, and so  
 CC replaces tacrolimus in the Edmonton protocol, thereby eliminating the  
 CC unwanted side effects of the calcineurin inhibitor. The present sequence  
 CC represents a CTLA4 mutant L104EA29LIg protein, which is used in an  
 CC example from the present invention.

XX Sequence 383 AA;

Query Match 98.8%; Score 649; DB 24; Length 383;  
 Best Local Similarity 99.2%; Pred. No. 1,2e-57;  
 Matches 124; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AMHVAOPAVYVLASSRGIAFVCEYASPGKTEVRVTVLRQADSQVTEVCATYMGNELT 60  
 DB 26 AMHVAOPAVYVLASSRGIAFVCEYASPGKTEVRVTVLRQADSQVTEVCATYMGNELT 85  
 QY 61 FLDDSICTGTSSGNQVNLTIQGLRAMDTGLYICKVELMPPPYEGIGNGTQIYVIDPEP 120  
 DB 86 FLDDSICTGTSSGNQVNLTIQGLRAMDTGLYICKVELMPPPYEGIGNGTQIYVIDPEP 145

QY 121 CPDSD 125  
 DB 146 CPDSD 150

RESULT 14  
 AAU75131 standard; Protein; 212 AA.

XX ID AAU75131;  
 XX 09-APR-2002 (first entry)  
 XX Human CTLA4 receptor mutant #6.  
 XX Human: Rheumatic disease; soluble cytotoxic T lymphocyte antigen 4; Ig;  
 KM CTLA4; variable (V)-like extracellular domain; CTLA4Ig; B7 molecule;  
 KM immunoglobulin constant domain; rheumatoid arthritis; autoimmune disease;  
 KM immune system disorder; graft-related disease; immunosuppressive; mutant;  
 KM immunoproliferative disease; antinflammatory; muten; receptor;  
 KM oncostatin M.  
 XX Homo sapiens.  
 OS Synthetic.

XX FH Key Location/Qualifiers  
 FT Peptide 1..26  
 FT Protein /label= Oncostatin\_M\_Signal\_peptide  
 FT 27..212  
 FT /label= Mature\_CTLA4\_receptor  
 FT Misc-difference 130  
 FT /note= "Substitution of wild type Leu to Glu"  
 PN WO200202638-A2.  
 PD 10-JAN-2002.  
 PF 02-JUL-2001; 2001WO-US21204.  
 XX 03-JUL-2000; 2000US-215913P.  
 XX (BRIM ) BRISTOL-MYERS SQUIBB CO.  
 XX Cohen R, Carr S, Hagerly D, Peach RJ, Becker J;  
 DR WPI; 2002-148002/19.  
 XX Composition useful for treating rheumatic disease and immune system  
 PT disorders e.g. diabetes mellitus, graft-related disease, good pasture's



PT syndrome, comprises soluble cytotoxic T lymphocyte A4 mutant molecule  
 PS Claim 12; Page -; 128pp; English.

CC The present invention relates to pharmaceutical compositions and  
 CC methods for treating rheumatic disease. The composition comprises a  
 CC soluble cytotoxic T lymphocyte antigen 4 (CTLA4) mutant molecule that  
 CC blocks endogenous B7 molecules from binding their ligands. Soluble  
 CC CTLA4 molecules are constructed by fusing variable (V)-like  
 CC extracellular domains of CTLA4 to immunoglobulin (Ig) constant domains  
 CC resulting in CTLA4Ig. The composition is useful for treating rheumatic  
 CC disease especially rheumatoid arthritis, and for alleviating a symptom  
 CC associated with a rheumatic disease from joint swelling, pain,  
 CC tenderness, and structural damage. The composition can optionally be used  
 CC with other pharmaceutical agents for treating immune system disorders  
 CC which include autoimmune diseases (e.g. systemic lupus erythematosus,  
 CC Addison's disease, diabetes mellitus, multiple sclerosis, Crohn's  
 CC disease, ulcerative colitis, Sjogren's syndrome, scleroderma and  
 CC sympathetic ophthalmia), graft-related diseases (e.g. graft-versus-host  
 CC disease), immunoproliferative diseases (e.g. psoriasis, T cell lymphoma,  
 CC Hashimoto's thyroiditis), pernicious anaemia and good pasture's syndrome).  
 CC The present sequence represents a mutant of the human CTLA4 receptor.  
 CC Note: The present sequence is not given in the patent but is created by  
 CC the indexer from the sequence provided in Fig 23 and the information  
 CC given in claim 12.

XX Sequence 212 AA;

Query Match

Best Local Similarity 98.6%; Score 648; DB 23; Length 212;

Matches 124; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AMHVAOPAVYVLASSRGISAFVCEYASPGKYTEYRTVLRQADSOYTEVCAATYMGNEIT 60

DB 26 AMHVAOPAVYVLASSRGISAFVCEYASPGKATEYRTVLRQADSOYTEVCAATYMGNEIT 85

QY 61 FLDDSICTGTSSGNOVNLTIQGLRAMDTGLYICKVELMPPPYEGIGNGTQIYVIDPEP 120

DB 86 FLDDSICTGTSSGNOVNLTIQGLRAMDTGLYICKVELMPPPYEGIGNGTQIYVIDPEP 145

QY 121 CPDSD 125

DB 146 CPDSD 150

RESULT 15

ABB78101

XX ABB78101 standard; Protein; 383 AA.

AC ABB78101;

DT 05-NOV-2002 (first entry)

DE Amino acid sequence of a CTLA4Ig mutant, designated L104E1g.

XX CTLA4Ig; mutant; L104E1g; CTLA4; immunoglobulin; Ig; B7;

KW immunosuppressive; mixed haematopoietic chimerism; transplanted tissue;

KW T cell depleted bone marrow cell; T cell costimulatory signal;

KW haemoglobinopathy; beta-thalassemia; sickle cell disease;

KW organ rejection.

XX Synthetic.

OS MO200258729-A2.

PN 01-AUG-2002.

PF 25-JAN-2002; 2002MO-US03780.

PR 26-JAN-2001; 2001US-264528P.

PR 05-JUL-2000; 2001US-303142P.

PA (UYEM-) UNIV EMORY.

XX Larsen CP, Pearson TC, Waller EK, Adams AB;

XX WPI; 2002-619143/66.

DR N-PSDB; ABQ78356.

PT Establishing mixed haematopoietic chimerism in subject after  
 PT transplantation, by administering T cell depleted bone marrow cells,  
 PT alkylating agent, immunosuppressive composition that blocks T cell  
 PT costimulatory signals -

PS Example 8; Fig 14; 161pp; English.

XX The present sequence represents a CTLA4Ig mutant, designated L104E1g.  
 CC CTLA4Ig is a soluble fusion protein, comprising an extracellular domain  
 CC of wild type CTLA4 joined to an immunoglobulin (Ig) tail or a portion  
 CC thereof which binds a B7 molecule. The present protein has the mutation  
 CC L104E. CTLA4Ig and its mutants are examples of immunosuppressive agents  
 CC that may be used in the method of the invention. The specification  
 CC describes a method of establishing mixed haematopoietic chimerism in  
 CC a subject with a transplanted tissue. The method comprises administering  
 CC to the subject, T cell depleted bone marrow cells, an alkylating agent  
 CC and an immunosuppressive composition that blocks T cell costimulatory  
 CC signals in the subject, thus establishing haematopoietic chimerism in the  
 CC subject. The method is useful for treating haemoglobinopathy  
 CC (e.g. beta-thalassemia or sickle cell disease), in a subject by  
 CC establishing haematopoietic chimerism. It is also useful for inhibiting  
 CC rejection of an organ or tissue transplanted into the subject.

XX Sequence 383 AA;

Query Match

Best Local Similarity 98.6%; Score 648; DB 23; Length 383;

Matches 124; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AMHVAOPAVYVLASSRGISAFVCEYASPGKYTEYRTVLRQADSOYTEVCAATYMGNEIT 60

DB 26 AMHVAOPAVYVLASSRGISAFVCEYASPGKATEYRTVLRQADSOYTEVCAATYMGNEIT 85

QY 61 FLDDSICTGTSSGNOVNLTIQGLRAMDTGLYICKVELMPPPYEGIGNGTQIYVIDPEP 120

DB 86 FLDDSICTGTSSGNOVNLTIQGLRAMDTGLYICKVELMPPPYEGIGNGTQIYVIDPEP 145

QY 121 CPDSD 125

DB 146 CPDSD 150

Search completed: August 23, 2003, 16:54:53  
 Job time : 61.5 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 23, 2003, 16:57:06 ; Search time 36 Seconds

(without alignments)  
458,200 Million cell updates/sec

Title: US-09-865-321a-4\_COPY\_26\_150  
Perfect score: 657  
Sequence: 1 AAHVAPAVYVLAASSRGIASF.....GIGNGTQIYIDPECPDSD 125

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 497079 seqs, 131961718 residues

Total number of hits satisfying chosen parameters: 497079

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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4: /cgn2\_6/ptodata/1/pubppa/US06\_PUBCOMB.pep:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	657	100.0	383	10	US-09-865-321-4
2	657	100.0	383	11	US-09-898-195A-9
3	657	100.0	383	15	US-10-057-288-4
4	657	100.0	383	15	US-10-155-514-6
5	652	99.2	383	11	US-09-898-195A-15
6	652	99.2	383	15	US-10-057-288-10
7	652	99.2	383	15	US-10-155-514-14
8	649	98.8	383	11	US-09-898-195A-11
9	649	98.8	383	15	US-10-057-288-6
10	649	98.8	383	15	US-10-155-514-10
11	648	98.6	383	11	US-09-865-321-6
12	648	98.6	383	11	US-09-898-195A-7
13	648	98.6	383	11	US-09-898-195A-13
14	648	98.6	383	15	US-10-057-288-2
15	648	98.6	383	15	US-10-057-288-8

16	648	98.6	383	15	US-10-155-514-8	Sequence 8, Appl1
17	648	98.6	383	15	US-10-155-514-12	Sequence 12, Appl1
18	640	97.4	151	15	US-10-207-655-309	Sequence 309, Appl
19	640	97.4	212	11	US-09-898-195A-17	Sequence 17, Appl1
20	640	97.4	212	15	US-10-057-288-12	Sequence 12, Appl1
21	640	97.4	212	15	US-10-155-514-2	Sequence 2, Appl1
22	640	97.4	374	14	US-10-027-075-26	Sequence 26, Appl1
23	640	97.4	374	14	US-10-027-075-28	Sequence 28, Appl1
24	640	97.4	377	15	US-10-027-075-24	Sequence 24, Appl1
25	640	97.4	382	15	US-10-207-655-307	Sequence 307, Appl
26	640	97.4	382	15	US-10-207-655-316	Sequence 316, Appl
27	640	97.4	383	10	US-09-865-321-8	Sequence 8, Appl1
28	640	97.4	383	11	US-09-898-195A-19	Sequence 19, Appl1
29	640	97.4	383	15	US-10-057-288-14	Sequence 14, Appl1
30	640	97.4	383	15	US-10-155-514-4	Sequence 4, Appl1
31	640	97.4	383	15	US-10-155-514-16	Sequence 16, Appl1
32	640	97.4	399	15	US-10-207-655-320	Sequence 320, Appl
33	640	97.4	403	15	US-10-207-655-318	Sequence 318, Appl
34	635	96.7	223	11	US-09-835-297-2	Sequence 2, Appl1
35	635	96.7	223	15	US-10-211-207-3	Sequence 3, Appl1
36	634	96.5	188	10	US-09-845-899A-7	Sequence 7, Appl1
37	634	96.5	223	15	US-09-989-545-21	Sequence 21, Appl1
38	634	96.5	223	15	US-10-225-519-8	Sequence 8, Appl1
39	634	96.5	223	15	US-10-207-655-101	Sequence 101, Appl
40	630	95.9	260	15	US-10-225-519-4	Sequence 4, Appl1
41	628	95.6	124	15	US-10-207-655-314	Sequence 314, Appl
42	627	95.4	187	11	US-09-014-761-1	Sequence 1, Appl1
43	627	95.4	223	14	US-10-107-828-26	Sequence 26, Appl1
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45	627	95.4	223	14	US-10-107-868-26	Sequence 26, Appl1

#### ALIGNMENTS

RESULT 1  
US-09-865-321-4  
; Sequence 4, Application US/09865321  
; Publication No. US20020182211A1  
; GENERAL INFORMATION:  
; APPLICANT: Peach, Robert J.  
; APPLICANT: Naemura, Joseph R.  
; APPLICANT: Insley, Peter S.  
; APPLICANT: Bajorth, Jürgen  
; TITLE OF INVENTION: SOLUBLE CTLA4 MUTANT MOLECULES AND USES THEREOF  
; FILE REFERENCE: DB2BWP/30436.57US01  
; CURRENT APPLICATION NUMBER: US/09/865,321  
; CURRENT FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: 60/287,576  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/214,065  
; PRIOR FILING DATE: 2000-06-26  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 383  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: L104EA29Y1g  
US-09-865-321-4

Query Match 100.0%; Score 657; DB 10; Length 383;  
Best Local Similarity 100.0%; Pred. No. 2.8e-61;  
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAHVAPAVYVLAASSRGIASFVCEYASPGKTEYRVTVLRQADSQVTEVCATYMGNEILT 60  
DB 26 AAHVAPAVYVLAASSRGIASFVCEYASPGKTEYRVTVLRQADSQVTEVCATYMGNEILT 85  
QY 61 FLDSDICTGTSSGNVNLFTIOGLRAMDTGLYICKVELMTPPYEIGNGTOIYVDPDP 120  
DB 86 FLDSDICTGTSSGNVNLFTIOGLRAMDTGLYICKVELMTPPYEIGNGTOIYVDPDP 145

QY	121	CPDSD	125
Db	146	CPDSD	150

RESULT 2  
ITS-09-A9

US-09-898-195A-9  
Sequence 9, Application US/09889195A  
Publication No. US20030083246A1  
GENERAL INFORMATION:  
APPLICANT: Cohen, Robert  
APPLICANT: Carr, Suzette  
APPLICANT: Hagerly, David  
APPLICANT: Hagerly, Robert J  
APPLICANT: Becker, Jean-Claude  
TITLE OF INVENTION: METHODS FOR TREATING RHEUMATIC DISEASES USING A SOLUBLE  
FILE REFERENCE: D0030NP/30436.55SU1  
CURRENT APPLICATION NUMBER: US/09/898,195A  
CURRENT FILING DATE: 2002-04-15  
PRIOR APPLICATION NUMBER: 60/215,913  
PRIOR FILING DATE: 2000-07-03  
NUMBER OF SEQ ID NOS: 19  
SOFTWARE: patentln Ver. 2.1  
SEQ ID NO 9  
LENGTH: 383  
TYPE: PRT  
ORGANISM: L104EA29Y1G  
US-09-898-195A-9

Query Match	100.0%	Score 657;	DB 11;	Length 383;
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QY	121	CPDSD	125	
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RESULT 3  
ITS-10-04

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US-10-057-288-4
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: Sequence 4, Application US/10057288
: Publication No. US20030007684A1
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: GENERAL INFORMATION:
:
: APPLICANT: Larsen, Christian P.
: APPLICANT: Pearson, Thomas C.
: APPLICANT: Waller, Edmund K.
: APPLICANT: Adams, Andrew B.
:
: TITLE OF INVENTION: METHODS OF INDUCING ORGAN TRANSPLANT TOLERANCE AND
:
: TITLE OF INVENTION: CORRECTING HEMOGLOBINOPATHIES
:
: FILE REFERENCE: D0136NP/30436.580SUI
:
: CURRENT APPLICATION NUMBER: US/10/057,288
:
: CURRENT FILING DATE: 2002-01-25
:
: PRIOR APPLICATION NUMBER: 60/264,528
:
: PRIOR FILING DATE: 2001-01-26
:
: PRIOR APPLICATION NUMBER: 60/203,142
:
: PRIOR FILING DATE: 2001-07-05
:
: NUMBER OF SEQ ID NOS: 20
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: SOFTWARE: PatentIn Ver. 2.1
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: SEQ ID NO 4
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: LENGTH: 383
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: TYPE: PRT
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: ORGANSIM: Artificial Sequence
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: FEATURE:
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; OTHER INFORMATION: Description of Artificial Sequence: L104EA29Y1g
; OTHER INFORMATION: sequence
US-10-057-288-4

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	Query Match	100.0%	Score 657	DB 15	length 383
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Db	26	AMHYAQPAYVLASSRGILASFVCEYASPEKYTEVRVTVLRLQADSOVTEYCAATYMMGNELT	85		
QY	61	FLDDISICTGTSSGNVNTITGRLAMDGLYICKYELMPPPYRSGISNGTIYVIDEPP	120		
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ITS-10-15

US-10-155-514-6  
 : Sequence 6, Application US/10155514  
 : Publication No. US20030022836A1  
 : GENERAL INFORMATION:  
 :  
 : APPLICANT: Larsen, Christian P.  
 : APPLICANT: Pearson, Thomas C.  
 : APPLICANT: Adams, Andrew B.  
 : TITLE OF INVENTION: METHODS FOR PROTECTING ALLOGENEIC ISLET TRANSPLANT USING SOLUBLE  
 : TITLE OF INVENTION: MUTANT MOLECULES  
 : FILE REFERENCE: D0173NP / 30436.620SU1  
 : CURRENT APPLICATION NUMBER: US/10/155,514  
 : CURRENT FILING DATE: 2002-09-06  
 : PRIOR APPLICATION NUMBER: 60/293,402  
 : PRIOR FILING DATE: 2001-05-23  
 : NUMBER OF SEQ ID NOS: 18  
 : SOFTWARE: PatentIn version 3.1  
 :  
 : SEQ ID NO 6  
 :  
 : LENGTH: 383  
 : TYPE: PRT  
 : ORGANISM: Artificial Sequence  
 : FEATURE:  
 : OTHER INFORMATION: Description of Artificial Sequence: L104En29Yt1g sequence  
 : US-10-155-514-6

Query Match	100.0%;	Score 657;	DB 15;	Length 383;
Best Local Similarity	100.0%;	Pred. No. 2.8e-61;		
Matches 125; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

	QY	Db	QY	QY	Db
1	AMHVAQPAVVLASSGSIASFVCEYASPGKYTEVRVTLVQAOASQVTEVCAATPMNGNELT	60			
26	AMHVAQPAVVLASSGSIASFVCEYASPGKYTEVRVTLVQAOASQVTEVCAATPMNGNELT	85			
61	FLDDSICTGSSGNQVNLITQGLRAMDTGLYCKVELMPPRYEGINGTOIYVIDPEP	120			
86	FLDDSICTGSSGNQVNLITQGLRAMDTGLYCKVELMPPRYEGINGTOIYVIDPEP	145			
121	CPDSD	125			
146	CPDSD	150			

## RESULT

```

US-09-898-155A-15
: Sequence 15, Application US/098981955A
: Publication No. US20030083246A1
:
: GENERAL INFORMATION:
:
: APPLICANT: Cohen, Robert
:
: APPLICANT: Carr, Suzette
:
: APPLICANT: Hagerty, David
:
: APPLICANT: Peach, Robert J
:
: APPLICANT: Becker, Jean-Claude

```

;; TITLE OF INVENTION: METHODS FOR TREATING RHEUMATIC DISEASES USING A SOLUBLE  
;; FILE REFERENCE: CT14 MOLECULE  
;; CURRENT APPLICATION NUMBER: US/09/898,195A  
;; PRIOR FILING DATE: 2002-04-15  
;; PRIOR APPLICATION NUMBER: 60/215,913  
;; NUMBER OF SEQ ID NOS: 19  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO 15  
;; LENGTH: 383  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Description of Artificial Sequence: L104EA29W1g  
US-09-898-195A-15

Query Match 99.2%; Score 652; DB 11; Length 383;  
Best Local Similarity 99.2%; Pred. No. 9.3e-61;  
Matches 124; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1 AMHYAOPAVVLAASRGISAFCEYASPEKTEVRYTVLRADSOVTEVCATYMMGNELT 60  
|||  
26 AMHYAOPAVVLAASRGISAFCEYASPEKTEVRYTVLRADSOVTEVCATYMMGNELT 85  
FLDSDICTGSSGNQVNLITIGLRAMDTGLYICKVELMPPPYEGIGNGTQIYVIDEP 120  
|||  
86 FLDSDICTGSSGNQVNLITIGLRAMDTGLYICKVELMPPPYEGIGNGTQIYVIDEP 145

QY 121 CPDSD 125  
|||  
Db 146 CPDSD 150

RESULT 6  
US-10-057-288-10  
;; Sequence 10, Application US/10057288  
;; Publication No. US20030007968A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Larsen, Christian P.  
;; APPLICANT: Pearson, Thomas C.  
;; APPLICANT: Waller, Edmund K.  
;; APPLICANT: Adams, Andrew B.  
;; TITLE OF INVENTION: METHODS OF INDUCING ORGAN TRANSPLANT TOLERANCE AND  
;; FILE REFERENCE: D0136NP/30436.580SU1  
;; CURRENT APPLICATION NUMBER: US/10/057,288  
;; PRIOR FILING DATE: 2002-01-25  
;; PRIOR APPLICATION NUMBER: 60/264,528  
;; PRIOR FILING DATE: 2001-01-26  
;; PRIOR APPLICATION NUMBER: 60/303,142  
;; PRIOR FILING DATE: 2001-07-05  
;; NUMBER OF SEQ ID NOS: 20  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO 10  
;; LENGTH: 383  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Description of Artificial Sequence: L104EA29W1g  
US-10-057-288-10

Query Match 99.2%; Score 652; DB 15; Length 383;  
Best Local Similarity 99.2%; Pred. No. 9.3e-61;  
Matches 124; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMHYAOPAVVLAASRGISAFCEYASPEKTEVRYTVLRADSOVTEVCATYMMGNELT 60  
|||  
26 AMHYAOPAVVLAASRGISAFCEYASPEKTEVRYTVLRADSOVTEVCATYMMGNELT 85  
FLDSDICTGSSGNQVNLITIGLRAMDTGLYICKVELMPPPYEGIGNGTQIYVIDEP 120  
|||  
61 FLSDSDICTGSSGNQVNLITIGLRAMDTGLYICKVELMPPPYEGIGNGTQIYVIDEP 120  
|||  
|||

Db 86 FLSDSDICTGSSGNQVNLITIGLRAMDTGLYICKVELMPPPYEGIGNGTQIYVIDEP 145  
|||  
QY 121 CPDSD 125  
|||  
Db 146 CPDSD 150

RESULT 7  
US-10-155-514-14  
;; Sequence 14, Application US/10155514  
;; Publication No. US20030022836A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Larsen, Christian P.  
;; APPLICANT: Pearson, Thomas C.  
;; APPLICANT: Adams, Andrew B.  
;; TITLE OF INVENTION: METHODS FOR PROTECTING ALLOGENEIC ISLET TRANSPLANT USING SOLU  
;; FILE REFERENCE: D0173NP / 30436.620SU1  
;; CURRENT APPLICATION NUMBER: US/10/155,514  
;; PRIOR FILING DATE: 2002-09-06  
;; PRIOR APPLICATION NUMBER: 60/293,402  
;; PRIOR FILING DATE: 2001-05-23  
;; NUMBER OF SEQ ID NOS: 18  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 14  
;; LENGTH: 383  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Description of Artificial Sequence: L104EA29W1g sequence  
US-10-155-514-14

Query Match 99.2%; Score 652; DB 15; Length 383;  
Best Local Similarity 99.2%; Pred. No. 9.3e-61;  
Matches 124; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMHYAOPAVVLAASRGISAFCEYASPEKTEVRYTVLRADSOVTEVCATYMMGNELT 60  
|||  
26 AMHYAOPAVVLAASRGISAFCEYASPEKTEVRYTVLRADSOVTEVCATYMMGNELT 85  
FLDSDICTGSSGNQVNLITIGLRAMDTGLYICKVELMPPPYEGIGNGTQIYVIDEP 120  
|||  
86 FLSDSDICTGSSGNQVNLITIGLRAMDTGLYICKVELMPPPYEGIGNGTQIYVIDEP 145

QY 121 CPDSD 125  
|||  
Db 146 CPDSD 150

RESULT 8  
US-09-898-195A-11  
;; Sequence 11, Application US/09898195A  
;; Publication No. US20030083246A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Cohen, Robert  
;; APPLICANT: Carr, Suzette  
;; APPLICANT: Hagerly, David  
;; APPLICANT: Beach, Robert J  
;; APPLICANT: Becker, Jean-Claude  
;; TITLE OF INVENTION: METHODS FOR TREATING RHEUMATIC DISEASES USING A SOLUBLE  
;; FILE REFERENCE: D0030NP/30436.550SU1  
;; CURRENT APPLICATION NUMBER: US/09/898,195A  
;; PRIOR FILING DATE: 2002-04-15  
;; PRIOR APPLICATION NUMBER: 60/215,913  
;; PRIOR FILING DATE: 2000-07-03  
;; NUMBER OF SEQ ID NOS: 19  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO 11  
;; LENGTH: 383  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:

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; OTHER INFORMATION: Description of Artificial Sequence: L104EA29Lig
US-09-898-195A-11
Query Match          98.8%; Score 649; DB 11; Length 383;
Best Local Similarity 99.2%; Pred. No. 1.9e-60;
Matches 124; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AMHVAQPAVVLASSRGIASFVCEYASPGKYTEVRVTVLRQADSOVTEVCATYMMGNELT 60
    |||||
DB 26 AMHVAQPAVVLASSRGIASFVCEYASPGKLTEVRVTVLRQADSOVTEVCATYMMGNELT 85
    |||||
QY 61 FLDDSICTGTSSGNQVNLTIQGLRAMDTGLYICKVELMPPPYEGIGNGTQIYVIDPEP 120
    |||||
DB 86 FLDDSICTGTSSGNQVNLTIQGLRAMDTGLYICKVELMPPPYEGIGNGTQIYVIDPEP 145
    |||||
QY 121 CPDSD 125
    |||||
DB 146 CPDSD 150

RESULT 9
US-10-057-288-6
; Sequence 6, Application US/10057288
; Publication No. US20030007968A1
; GENERAL INFORMATION:
; APPLICANT: Larsen, Christian P.
; APPLICANT: Pearson, Thomas C.
; APPLICANT: Waller, Edmund K.
; APPLICANT: Adams, Andrew B.
; TITLE OF INVENTION: METHODS OF INDUCING ORGAN TRANSPLANT TOLERANCE AND
; FILE REFERENCE: D0136NP/30436.58US01
; CURRENT APPLICATION NUMBER: US/10/057,288
; CURRENT FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: 60/264,528
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/303,142
; PRIOR FILING DATE: 2001-07-05
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 6
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: L104EA29Lig
US-10-057-288-6
Query Match          98.8%; Score 649; DB 15; Length 383;
Best Local Similarity 99.2%; Pred. No. 1.9e-60;
Matches 124; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AMHVAQPAVVLASSRGIASFVCEYASPGKYTEVRVTVLRQADSOVTEVCATYMMGNELT 60
    |||||
DB 26 AMHVAQPAVVLASSRGIASFVCEYASPGKLTEVRVTVLRQADSOVTEVCATYMMGNELT 85
    |||||
QY 61 FLDDSICTGTSSGNQVNLTIQGLRAMDTGLYICKVELMPPPYEGIGNGTQIYVIDPEP 120
    |||||
DB 86 FLDDSICTGTSSGNQVNLTIQGLRAMDTGLYICKVELMPPPYEGIGNGTQIYVIDPEP 145
    |||||
QY 121 CPDSD 125
    |||||
DB 146 CPDSD 150

RESULT 10
US-10-155-514-10
; Sequence 10, Application US/10155514
; Publication No. US20030022836A1
; GENERAL INFORMATION:
; APPLICANT: Larsen, Christian P.
; APPLICANT: Pearson, Thomas C.

; APPLICANT: Adams, Andrew B.
; TITLE OF INVENTION: METHODS FOR PROTECTING ALLOGENEIC ISLET TRANSPLANT USING SOLUB
; FILE REFERENCE: D0173NP / 30436.62US01
; CURRENT APPLICATION NUMBER: US/10/155,514
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: 60/293,402
; PRIOR FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 10
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: L104EA29Lig sequence
US-10-155-514-10
Query Match          98.8%; Score 649; DB 15; Length 383;
Best Local Similarity 99.2%; Pred. No. 1.9e-60;
Matches 124; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AMHVAQPAVVLASSRGIASFVCEYASPGKYTEVRVTVLRQADSOVTEVCATYMMGNELT 60
    |||||
DB 26 AMHVAQPAVVLASSRGIASFVCEYASPGKLTEVRVTVLRQADSOVTEVCATYMMGNELT 85
    |||||
QY 61 FLDDSICTGTSSGNQVNLTIQGLRAMDTGLYICKVELMPPPYEGIGNGTQIYVIDPEP 120
    |||||
DB 86 FLDDSICTGTSSGNQVNLTIQGLRAMDTGLYICKVELMPPPYEGIGNGTQIYVIDPEP 145
    |||||

RESULT 11
US-09-865-321-6
; Sequence 6, Application US/09865321
; Publication No. US20020182211A1
; GENERAL INFORMATION:
; APPLICANT: Peach, Robert J.
; APPLICANT: Naemura, Joseph R.
; APPLICANT: Linsley, Peter S.
; APPLICANT: Bajorath, Jürgen
; TITLE OF INVENTION: SOLUBLE CTLA4 MUTANT MOLECULES AND USES THEREOF
; FILE REFERENCE: DB28NP/30436.57US01
; CURRENT APPLICATION NUMBER: US/09/865,321
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/287,576
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/214,065
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 6
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: L104E1g
US-09-865-321-6
Query Match          98.6%; Score 648; DB 10; Length 383;
Best Local Similarity 99.2%; Pred. No. 2.5e-60;
Matches 124; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AMHVAQPAVVLASSRGIASFVCEYASPGKYTEVRVTVLRQADSOVTEVCATYMMGNELT 60
    |||||
DB 26 AMHVAQPAVVLASSRGIASFVCEYASPGKYTEVRVTVLRQADSOVTEVCATYMMGNELT 85
    |||||
QY 61 FLDDSICTGTSSGNQVNLTIQGLRAMDTGLYICKVELMPPPYEGIGNGTQIYVIDPEP 120
    |||||
DB 86 FLDDSICTGTSSGNQVNLTIQGLRAMDTGLYICKVELMPPPYEGIGNGTQIYVIDPEP 145
    |||||
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OTHER INFORMATION: Description of Artificial Sequence: L104EA29Tig

APPLICANT: Larsen, Christian P

APPLICANT: Waller, Edmund K.

APPLICANT: Adams, Andrew B.  
TITLE OF INVENTION: METHODS OF INDUCING ORGAN TRANSPLANT TOLERANCE AND  
FILE REFERENCE: D0136NP/30436.58US01  
CURRENT APPLICATION NUMBER: US/10/057,288  
CURRENT FILING DATE: 2002-01-25  
PRIOR APPLICATION NUMBER: 60/264,528  
PRIOR FILING DATE: 2001-01-26  
PRIOR APPLICATION NUMBER: 60/303,142  
PRIOR FILING DATE: 2001-07-05  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 8  
LENGTH: 383  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: L104EA29Fig  
US-10-057-288-8

Query Match 98.6%; Score 648; DB 15; Length 383;  
Best Local Similarity 99.2%; Pred. No. 2.5e-60;  
Matches 124; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AMHVAQPAYVLASSRGVAFVCEYASPGKYTEVRVTVLRQADSOVTEVCATYTMGNELT 60  
Db 26 AMHVAQPAYVLASSRGVAFVCEYASPGKYTEVRVTVLRQADSOVTEVCATYTMGNELT 85  
QY 61 FLDDSICTGTSSGNQVNLTIQGLRAMDTGLYICKVELMYPYPYEGISGNGTQIYVIDPEP 120  
Db 86 FLDDSICTGTSSGNQVNLTIQGLRAMDTGLYICKVELMYPYPYEGISGNGTQIYVIDPEP 145  
QY 121 CPDSD 125  
Db 146 CPDSD 150

Search completed: August 23, 2003, 17:09:43  
Job time : 37 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 23, 2003, 16:52:21 ; Search time 20.5 Seconds

(Without alignments)  
257,993 Million cell updates/sec

Title: US-09-865-321a-4\_COPY\_26\_150

Sequence: 1 AMHVAQPAVVLASRGIAASF.....GICNGIQIYIDPEPCDSD 125

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_AA.\*  
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2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/1aa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/1aa/PCFUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/1aa/Backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	640	97.4	187	1 US-08-067-684-14	Sequence 14, Appl
2	640	97.4	187	1 US-08-008-898-14	Sequence 14, Appl
3	640	97.4	187	2 US-08-459-818-14	Sequence 14, Appl
4	640	97.4	187	2 US-08-889-666-14	Sequence 14, Appl
5	640	97.4	187	2 US-08-465-078-14	Sequence 14, Appl
6	640	97.4	187	2 US-08-725-776-14	Sequence 14, Appl
7	640	97.4	187	2 US-08-488-062-14	Sequence 14, Appl
8	640	97.4	187	3 US-08-228-208A-14	Sequence 14, Appl
9	640	97.4	223	3 US-08-228-208A-17	Sequence 17, Appl
10	640	97.4	374	4 US-09-227-595-26	Sequence 26, Appl
11	640	97.4	374	4 US-09-227-595-28	Sequence 26, Appl
12	640	97.4	377	4 US-09-227-595-24	Sequence 26, Appl
13	637	97.0	187	5 PCT-US95-06726-36	Sequence 24, Appl
14	631	96.0	124	3 US-08-630-172-4	Sequence 36, Appl
15	631	96.0	124	3 US-09-375-419-4	Sequence 4, Appl
16	631	96.0	357	3 US-08-630-172-20	Sequence 20, Appl
17	631	96.0	357	3 US-09-375-419-20	Sequence 20, Appl
18	617.5	94.0	253	2 US-08-459-818-20	Sequence 20, Appl
19	617.5	94.0	253	2 US-08-889-666-20	Sequence 20, Appl
20	617.5	94.0	253	2 US-08-465-078-20	Sequence 20, Appl
21	617.5	94.0	253	2 US-08-725-776-20	Sequence 20, Appl
22	617.5	94.0	253	2 US-08-488-062-20	Sequence 20, Appl
23	617.5	94.0	502	2 US-08-459-818-19	Sequence 19, Appl
24	617.5	94.0	502	2 US-08-889-666-19	Sequence 19, Appl
25	617.5	94.0	502	2 US-08-465-078-19	Sequence 19, Appl
26	617.5	94.0	502	2 US-08-725-776-19	Sequence 19, Appl
27	617.5	94.0	502	2 US-08-488-062-19	Sequence 19, Appl

28	602	91.6	234	1 US-08-505-058-1	Sequence 1, Appl
29	602	91.6	234	2 US-08-459-818-21	Sequence 21, Appl
30	602	91.6	234	2 US-08-889-666-21	Sequence 21, Appl
31	602	91.6	234	2 US-08-465-078-21	Sequence 21, Appl
32	602	91.6	234	2 US-08-725-776-21	Sequence 21, Appl
33	602	91.6	234	3 US-08-488-062-21	Sequence 21, Appl
34	584	88.9	137	3 US-08-804-180C-2	Sequence 2, Appl
35	570	86.8	238	4 US-09-227-595-30	Sequence 30, Appl
36	570	86.8	238	4 US-09-227-595-32	Sequence 32, Appl
37	550	83.7	109	4 US-09-460-384-34	Sequence 34, Appl
38	541	82.3	223	4 US-09-303-040-10	Sequence 10, Appl
39	434	66.1	223	3 US-08-228-208A-18	Sequence 18, Appl
40	420	63.9	174	3 US-08-804-180C-4	Sequence 4, Appl
41	404	61.5	234	1 US-08-505-058-2	Sequence 2, Appl
42	404	61.5	234	2 US-08-459-818-22	Sequence 22, Appl
43	404	61.5	234	2 US-08-889-666-22	Sequence 22, Appl
44	404	61.5	234	2 US-08-465-078-22	Sequence 22, Appl
45	404	61.5	234	2 US-08-725-776-22	Sequence 22, Appl

## ALIGNMENTS

RESULT 1  
US-08-067-684-14  
Sequence 14, Application US/08067684  
Patent No. 5434131

GENERAL INFORMATION:

APPLICANT: Linsley, Peter S.  
APPLICANT: Ledbetter, Jeffrey A.

APPLICANT: Damle, Nitin K.  
APPLICANT: Brady, William

TITLE OF INVENTION: CTLA4 RECEPTOR AND METHODS FOR ITS USE  
NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:  
ADDRESS: Sheldon & Mak  
STREET: 225 South Lake Avenue, Suite 900

CITY: Pasadena  
STATE: California

COUNTRY: U.S.A.  
ZIP: 91101

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/067,684  
FILING DATE: 26-MAY-1993

CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Adriano, Sarah B.

REGISTRATION NUMBER: 34,470  
REFERENCE/DOCKET NUMBER: 7848-1

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 310/312-0900  
TELEFAX: 310/479-8340

INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 187 amino acids

TYPE: amino acid  
MOLECULE TYPE: protein  
HYPOTHEICAL: NO

ANTI-SENSE: NO  
US-08-067-684-14

Query Match

Best Local Similarity 97.4%; Score 640; DB 1; Length 187;  
Matches 123; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 AMHVAQPAVVLASRGIAASFCEYASPGKTEVTVLRADSOVTEVCATYMGNELT 60  
|||||



Db 1 AMHVAQPAVVLASSRGISAFVCEYASPGKATEVRVTVLRQADSQVTEVCATYMMGNELT 60  
QY 61 FLDSDICGTSSGNQVNLITQGLRAMDGLTYCKVELMPPPYEGISGNGTOIYYIDPEP 120  
Db 61 FLDSDICGTSSGNQVNLITQGLRAMDGLTYCKVELMPPPYEGISGNGTOIYYIDPEP 120  
QY 121 CPDSD 125  
Db 121 CPDSD 125

## RESULT 2

US-08-008-898-14  
; Sequence 14, Application US/08008898  
; Patent No. 5770197  
; GENERAL INFORMATION:  
; APPLICANT: Linsley, Peter S  
; APPLICANT: Ledbetter, Jeffrey A  
; APPLICANT: Damle, Milton K  
; APPLICANT: Brady, William  
; TITLE OF INVENTION: CTLA4 RECEPTOR AND METHODS FOR ITS USE  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sheldon & Mak  
; STREET: 201 South Lake Avenue, Suite 800  
; CITY: Pasadena  
; STATE: California  
; COUNTRY: United States  
; ZIP: 91101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/008,898  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/723,617  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mandel, Saralynn  
; REGISTRATION NUMBER: 31,853  
; REFERENCE/DOCKET NUMBER: 7848  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (818) 796-4000  
; TELEFAX: (818) 795-6321  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 187 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-008-898-14

Query Match 97.4%; Score 640; DB 1; Length 187;  
Best Local Similarity 98.4%; Pred. No. 66-65;  
Matches 123; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AMHVAQPAVVLASSRGISAFVCEYASPGKATEVRVTVLRQADSQVTEVCATYMMGNELT 60  
Db 1 AMHVAQPAVVLASSRGISAFVCEYASPGKATEVRVTVLRQADSQVTEVCATYMMGNELT 60  
QY 61 FLDSDICGTSSGNQVNLITQGLRAMDGLTYCKVELMPPPYEGISGNGTOIYYIDPEP 120  
Db 61 FLDSDICGTSSGNQVNLITQGLRAMDGLTYCKVELMPPPYEGISGNGTOIYYIDPEP 120  
QY 121 CPDSD 125  
Db 121 CPDSD 125

## RESULT 3

US-08-459-818-14  
; Sequence 14, Application US/08459818  
; Patent No. 5851795  
; GENERAL INFORMATION:  
; APPLICANT: Linsley, Peter S.  
; APPLICANT: Ledbetter, Jeffrey A.  
; APPLICANT: Damle, Milton K.  
; APPLICANT: Brady, William  
; TITLE OF INVENTION: CTLA4 Receptor and Uses Thereof  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merchant & Gould  
; STREET: 1150 Santa Monica Blvd., Suite 400  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: USA  
; ZIP: 90025  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: FastSeq 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/459,818  
; FILING DATE: 02-JUN-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Adriano, Sarah B.  
; REGISTRATION NUMBER: 34,470  
; REFERENCE/DOCKET NUMBER: 30436.35US02  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 310-445-1140  
; TELEFAX: 310-445-9031  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 187 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-459-818-14

Query Match 97.4%; Score 640; DB 2; Length 187;  
Best Local Similarity 98.4%; Pred. No. 66-65;  
Matches 123; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AMHVAQPAVVLASSRGISAFVCEYASPGKATEVRVTVLRQADSQVTEVCATYMMGNELT 60  
Db 1 AMHVAQPAVVLASSRGISAFVCEYASPGKATEVRVTVLRQADSQVTEVCATYMMGNELT 60  
QY 61 FLDSDICGTSSGNQVNLITQGLRAMDGLTYCKVELMPPPYEGISGNGTOIYYIDPEP 120  
Db 61 FLDSDICGTSSGNQVNLITQGLRAMDGLTYCKVELMPPPYEGISGNGTOIYYIDPEP 120  
QY 121 CPDSD 125  
Db 121 CPDSD 125

## RESULT 4

US-08-889-666-14  
; Sequence 14, Application US/08889666  
; Patent No. 5885579  
; GENERAL INFORMATION:  
; APPLICANT: Linsley, Peter S.  
; APPLICANT: Ledbetter, Jeffrey A.  
; APPLICANT: Damle, Milton K.  
; APPLICANT: Brady, William  
; APPLICANT: Kiener, Peter A.  
; TITLE OF INVENTION: CTLA4 Receptor and Uses Thereof  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merchant & Gould

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OM protein - protein search, using sw model

Run on: August 23, 2003, 16:50:56 ; Search time 24.5 Seconds

(without alignments)  
490.657 Million cell updates/sec

Title: US-09-865-321a-8\_COPY\_26\_150

Sequence: 1 AMHYAOPAVVIASSRGIA SF.....GIGNGTQIYVIDPEPCDSD 125

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 segs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR\_76:\*  
2: PIR1:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	647	99.1	223	2	T09536
2	644	98.6	186	2	S08614
3	561	85.9	223	2	I46696
4	458	70.1	223	2	A29063
5	150	23.0	221	2	S25168
6	139	21.3	173	2	I46197
7	127.5	19.5	220	1	RWHU28
8	121	18.5	221	2	I46689
9	121	17.5	218	2	A43523
10	114	15.4	218	2	S24413
11	100.5	15.4	120	2	S46370
12	99	15.2	124	2	S40336
13	95.5	14.6	108	2	S36277
14	95.5	14.6	132	2	S38646
15	94.5	14.5	140	2	PL0013
16	94	14.4	125	2	S40353
17	93.5	14.3	128	2	S46372
18	93	14.2	108	2	S30521
19	92.5	14.2	117	2	S46371
20	92.5	14.2	117	2	S46371
21	91	13.9	213	2	A21177
22	90.5	13.9	132	2	S40353
23	90	13.8	111	2	S36281
24	89.5	13.7	105	2	S26338
25	89	13.6	111	2	S38497
26	89	13.6	112	2	H26317
27	88.5	13.6	108	2	S36279
28	88	13.5	111	1	L2HUTG
29	88	13.5	111	1	L2HUTR

30	87.5	13.4	123	2	S40378	Ig kappa chain - h
31	87	13.3	92	2	S37504	Ig kappa chain V r
32	87	13.3	104	2	UC6076	anti-D-dimer monoc
33	87	13.3	108	2	S34007	Ig kappa chain V r
34	87	13.3	112	2	PL0274	Ig kappa chain V r
35	86.5	13.2	107	2	S12954	Ig kappa chain V r
36	86	13.2	92	2	S37516	Ig kappa chain V r
37	86	13.2	111	2	S19671	Ig kappa chain V
38	86	13.2	129	2	S40369	Ig kappa chain - h
39	85.5	13.1	124	2	S40318	Ig kappa chain V r
40	85.5	13.1	125	2	S40350	Ig kappa chain - h
41	85.5	13.1	212	2	S70431	Ig kappa chain - h
42	85.5	13.1	235	2	S14675	Ig kappa chain -
43	84.5	12.9	108	2	G44151	Ig kappa chain V r
44	84.5	12.9	110	2	S60591	Ig light chain var
45	84.5	12.9	111	2	PM0537	Ig kappa chain V r

#### ALIGNMENTS

```

RESULT 1
T09536
cytotoxic T-lymphocyte protein 4 - human
C:Species: Homo sapiens (man)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C:Accession: T09536
R:Harper, K.; Balzano, C.; Rouvler, E.; Mattei, M.G.; Luciani, M.F.; Golstein, P.
J. Immunol. 147, 1037-1044, 1991
A:Title: CTLA-4 and CD28 activated lymphocyte molecules are closely related in both n
A:Reference number: I49584; MUID:91318145; PMID:1713603
A:Accession: T09536
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-223 <HAR>
A:Cross-references: EMBL:LI5006; NID:9291928; PIDN:AA859385.1; PID:9291929
C:Genetics:
A:Gene: CTLA4
A:Map position: 2q33
C:Superfamily: T-cell surface glycoprotein CD28; immunoglobulin homology
C:Keywords: T-cell; transmembrane protein

Query Match          99.1% Score 647; DB 2; Length 223;
Best Local Similarity 99.2% Pred. NO. 3e-57;
Matches 124; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY      1 AMHYAOPAVVIASSRGIA SFCEYASPKATEVRYTLRDSDQVTEVCATYMMGNELT 60
        |||||
DB      37 AMHYAOPAVVIASSRGIA SFCEYASPKATEVRYTLRDSDQVTEVCATYMMGNELT 96
        |||||

OY      61 FLDSICTGTSSGNQVNLITGLRAMDTGIXICKEVELMYPPIYLGIGNGTQIYVIDPEP 120
        |||||
DB      97 FLDSICTGTSSGNQVNLITGLRAMDTGIXICKEVELMYPPIYLGIGNGTQIYVIDPEP 156
        |||||

OY      121 CPDSD 125
        |||||
DB      157 CPDSD 161
        |||||

RESULT 2
S08614
cytotoxic T-lymphocyte protein 4 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 11-Jan-2000
C:Accession: S08614
R:Darlavach, P.; Mattei, M.G.; Golstein, P.; Letfranc, M.P.
Eur. J. Immunol. 18, 1901-1905, 1988
A:Title: Human Ig superfamily CTLA-4 gene: chromosomal localization and identity of p
A:Reference number: S08614; MUID:89120925; PMID:3220103
A:Accession: S08614
A:Molecule type: DNA
A:Residues: 1-186 <DAR>
A:Cross-references: EMBL:X15070; NID:930283; PID:9825649

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OW protein - protein search, using sw model

Run on: August 23, 2003, 16:43:01 ; Search time 13.5 Seconds

435.432 Million cell updates/sec

Title: US-09-865-321a-8\_COPY\_26\_150  
Sequence: 1 AMHVACPAVVIASSRGIAASF.....GICNGTQIYIDPEPCDSD 125

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	653	100.0	223	1	CTLA4_HUMAN
2	561	85.9	223	1	CTLA4_RABIT
3	558	85.5	223	1	CTLA4_PIG
4	458	70.1	223	1	CTLA4_MOUSE
5	150	23.0	221	1	CD28_CHICK
6	129.5	19.8	219	1	CD28_BOVIN
7	127.5	19.5	220	1	CD28_HUMAN
8	127.5	19.5	221	1	CD28_RABIT
9	121	18.5	218	1	CD28_MOUSE
10	114	17.5	218	1	CD28_RAT
11	88	13.5	111	1	LV2A_HUMAN
12	88	13.5	111	1	LV2D_HUMAN
13	85	13.0	480	1	SAHH_XANCP
14	83.5	12.8	108	1	SAHH_HUMAN
15	83	12.7	111	1	RV12_RABIT
16	83	12.7	739	1	VCAL_RAT
17	81	12.4	109	1	LV2E_HUMAN
18	80.5	12.3	108	1	VC1G_HUMAN
19	80.5	12.3	108	1	KV6C_MOUSE
20	80.5	12.3	109	1	KV6I_RAT
21	79.5	12.2	3707	1	PGBM_MOUSE
22	78.5	12.0	113	1	RV2C_MOUSE
23	78.5	12.0	149	1	RV5A_MOUSE
24	78	11.9	111	1	LV2H_MOUSE
25	78	11.9	480	1	SAHH_XANAC
26	78	11.9	480	1	SAHH_XANCP
27	78	11.9	485	1	SAHH_XYLFA
28	78	11.9	739	1	VCAL_MESCR
29	77.5	11.9	113	1	VC1G_MOUSE
30	77	11.8	111	1	LV2C_MOUSE
31	77	11.8	129	1	LV2F_HUMAN
32	77	11.8	715	1	LOC1_LACTA
33	77	11.8	4391	1	PGBM_HUMAN

34	76.5	11.7	111	1	LV2L_HUMAN	P80422 homo sapien
35	76.5	11.7	466	1	SAHH_BRUME	O8ye49 bruceella me
36	76	11.6	109	1	RV3E_HUMAN	P01624 homo sapien
37	76	11.6	112	1	RV2D_MOUSE	P01623 mus musculu
38	76	11.6	114	1	RV4A_HUMAN	P01625 homo sapien
39	75.5	11.6	463	1	SAHH_CAUCR	O9ab0 caulobacter
40	75.5	11.6	485	1	SAHH_WHEAT	P32113 triticum ae
41	75	11.5	106	1	LV4B_HUMAN	P01716 homo sapien
42	75	11.5	109	1	RV4D_HUMAN	P83593 homo sapien
43	75	11.5	112	1	LV6B_HUMAN	P01722 homo sapien
44	74.5	11.4	107	1	RV6B_MOUSE	P01676 mus musculu
45	74.5	11.4	108	1	RV1V_HUMAN	P04430 homo sapien

## ALIGNMENTS

RESULT 1	CTLA4_HUMAN	STANDARD:	PRT:	223 AA.
AC	P16410: Q8WXL1; Q96P43; Q9UKN9;			
DT	01-AUG-1990 (Rel. 15, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Cytotoxic T-lymphocyte protein 4 precursor (Cytotoxic T-lymphocyte-associated antigen 4) (CTLA-4) (CD152 antigen).			
GN	CTLA4 OR CD152.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=21601151; PubMed=11735222;			
RA	Ling V., Wu P.W., Finnerty H.F., Agostino M.J., Graham J.R., Chen S.,			
RT	Jussif J., Fisk G.J., Miller C.P., Collins M.;			
RT	"Assembly and annotation of human chromosome 2q33 sequence containing			
RT	the CD28, CTLA4, and ICOS gene cluster: analysis by computational,			
RT	comparative, and microarray approaches.";			
RL	Genomics 78:155-168(2001).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	Mu P.W., Ling V.;			
RA	"Full length sequence of hCTLA4 cDNA.";			
RT	Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.			
RN	[3]			
RP	SEQUENCE OF 1-37 FROM N.A.			
RX	MEDLINE=91318145; PubMed=1713603;			
RA	Harper K., Balzano C., Rouvier E., Mattei M.-G., Luciani M.F.,			
RT	Golstein P.;			
RT	"CTLA-4 and CD28 activated lymphocyte molecules are closely related			
RT	in both mouse and human as to sequence, message expression, gene			
RT	structure, and chromosomal location.";			
RL	J. Immunol. 147:1037-1044(1991).			
RN	[4]			
RP	SEQUENCE OF 38-223 FROM N.A.			
RX	TISSUE-Lymphocytes;			
RA	MEDLINE=99120925; PubMed=3220103;			
RT	Darivach P., Mattei M.-G., Golstein P., Lefranc M.-P.;			
RT	"Human Ig superfamily CTLA-4 gene: chromosomal localization and			
RT	identity of protein sequence between murine and human CTLA-4			
RT	cytoplasmic domains.";			
RL	Eur. J. Immunol. 18:1901-1905(1988).			
RN	[5]			
RP	SEQUENCE OF 140-223 FROM N.A., AND TISSUE SPECIFICITY.			
RX	MEDLINE=99425274; PubMed=10493833;			
RA	Ling V., Wu P.W., Finnerty H.F., Sharpe A.H., Gray G.S., Collins M.;			
RT	"Complete sequence determination of the mouse and human CTLA4 gene			
RT	loci: cross-species DNA sequence similarity beyond exon borders.";			
RL	Genomics 60:341-355(1999).			
RN	[6]			
RP	FUNCTION.			
RX	MEDLINE=91341416; PubMed=1714933;			

RA Linsley P.S., Brady W., Urnes M., Grismaire L.S., Damle N.K.,  
RA Ledbetter J.A.,  
RT "CTLA-4 is a second receptor for the B cell activation antigen B7.",  
RL J. Exp. Med. 174:561-569(1991).  
RN [7]  
RP STRUCTURE BY NMR OF 37-165.  
RX MEDLINE-97317889; PubMed-9228944;  
RA Metzler W.J., Bajorath J., Fenderson W., Shaw S.Y., Constantine K.L.,  
RA Naemura J., Leytze G., Peach R.J., Lawle T.B., Mueller L.,  
RA Linsley P.S.,  
RT "Solution structure of human CTLA-4 and delineation of a CD80/CD86  
RT binding site conserved in CD28.",  
RL Nat. Struct. Biol. 4:527-531(1997).  
RN [8]  
RP VARIANT ALA-17, AND ASSOCIATION WITH IDDM2.  
RX MEDLINE-97402209; PubMed-9259273;  
RA Marron M.P., Raffel L.J., Garchon H.-J., Jacob C.O., Serrano-Rios M.,  
RA Martinez Larraz M.T., Teng W.-P., Park Y., Zhang Z.-X.,  
RA Goldstein D.R., Tao Y.-W., Beauvain G., Bach J.-F., Huang H.-S.,  
RA Luo D.-F., Zeller A., Rotter J.I., Yang M.C.K., Modilevsky T.,  
RA MacLaren N.K., She J.-X.,  
RT "Insulin-dependent diabetes mellitus (IDDM) is associated with CTLA4  
RT polymorphisms in multiple ethnic groups.",  
RL Hum. Mol. Genet. 6:1275-1282(1997).  
RN [9]  
RP POLYMORPHISM, AND ASSOCIATION WITH COELIAC DISEASE.  
RX MEDLINE-99205840; PubMed-10189842;  
RA Djilali-Saiah I., Schmitz J., Harfouch-Hamoud E., Mougnot J.-F.,  
RA Bach J.-F., Gallat-Zucman S.,  
RT "CTLA-4 gene polymorphism is associated with predisposition to coeliac  
RT disease.",  
RL Gut 43:187-189(1996).  
RN [10]  
RP VARIANT ALA-17, AND ASSOCIATION WITH TAO.  
RX MEDLINE-99402177; PubMed-10475192;  
RA Vaidya B., Imiri H., Perros P., Dickinson J., McCarthy M.I.,  
RA Kendall-Taylor P., Pearce S.H.S.,  
RT "Cytotoxic T lymphocyte antigen-4 (CTLA-4) gene polymorphism confers  
RT susceptibility to thyroid associated orbitopathy.",  
RL Lancet 354:743-744(1999).  
RN [11]  
RP VARIANT ALA-17, AND ASSOCIATION WITH GRD.  
RX MEDLINE-20385252; PubMed-10924276;  
RA Chistyakov D.A., Savost'ancov K.V., Turakulov R.I., Petulina N.A.,  
RA Trukhina L.V., Kudanova A.V., Balabokhin M.I., Nosikov V.V.,  
RT "Complex association analysis of Graves disease using a set of  
RT polymorphic markers.",  
RL Mol. Genet. Metab. 70:214-218(2000).  
RN [12]  
RP VARIANT ALA-17.  
RX MEDLINE-20395844; PubMed-10903931;  
RA Deng Z., Morse J.H., Slager S.L., Cuervo N., Moore K.J., Venetos G.,  
RA Kalachikov S., Cayanis E., Fischer S.G., Barst R.J., Hodge S.E.,  
RA Knowles J.A.,  
RT "Familial primary pulmonary hypertension (gene PPH1) is caused by  
RT mutations in the bone morphogenetic protein receptor-II gene.",  
RL Am. J. Hum. Genet. 67:737-744(2000).  
RN [13]  
RP -1- FUNCTION: POSSIBLY INVOLVED IN T-CELL ACTIVATION. BINDS TO B7-1  
RP (CD80) AND B7-2 (CD86).  
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -1- TISSUE SPECIFICITY: Widely expressed with highest levels in  
CC lymphoid tissues.  
CC -1- POLYMORPHISM: The variant Ala-17 is associated with an increased  
CC risk for autoimmune disorders as Graves disease (GRD), type I  
CC insulin-dependent diabetes mellitus (IDDM2), and thyroid-  
CC associated orbitopathy (TAO). The variant Thr-17 is associated  
CC with predisposition to coeliac disease, a gluten sensitive  
CC enteropathy characterized by small bowel mucosal atrophy.  
CC -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.  
CC -1- DATABASE: NAME=PROV; NOTE=CD guide CD152 entry;  
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd152.htm".  
CC  
CC THIS SWISS-PROT entry is copyright It is produced through a collaboration

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or send an email to license@isb.slb.ch).  
CC -----  
DR EMBL; AF411058; AAL40932.1; -;  
DR EMBL; AF414120; AAL07473.1; -;  
DR EMBL; M73463; AAA52127.1; -;  
DR EMBL; M37245; AAA52773.1; JOINED.  
DR EMBL; M37243; AAA52773.1; JOINED.  
DR EMBL; M37244; AAA52773.1; JOINED.  
DR EMBL; AF142144; AAF02499.1; -;  
DR PIR; S08614; S08614.  
DR PDB; 1AH1; 15-APR-98.  
DR PDB; 1HGF; 28-NOV-01.  
DR PDB; 1I85; 04-APR-01.  
DR PDB; 1IBL; 04-APR-01.  
DR Genew; HGNC:2505; CTIA4.  
DR MIM; 123890; -;  
DR GO; GO:0005887; C:Integral to plasma membrane; TAS.  
DR GO; GO:0006955; P:Immune response; TAS.  
DR InterPro; IPR003596; Ig_V.  
DR SMART; SM00409; IG_1.  
DR SMART; SM00406; IGv_1.  
DR PROSITE; PS50835; IG_LIKE; FALSE_NEG.  
KW Immunoglobulin domain; T-cell; Transmembrane; Glycoprotein; Signal;  
KW 3D-structure; Polymorphism.  
FT SIGNAL          1      35     POTENTIAL.  
FT CHAIN           36      223    CYTOTOXIC T-LYMPHOCYTE PROTEIN 4.  
FT DOMAIN          36      161    EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM       162      187    POTENTIAL.  
FT DOMAINS        188      223    CYTOPLASMIC (POTENTIAL).  
FT DOMAIN         39      140    IG-LIKE V-TYPE.  
FT DISULFID       58      129  
FT DISULFID       85      103  
FT CARBOHYD       113      113  
FT VARIANT         17      17     N-LINKED (GLCNAC... ) (POTENTIAL).  
FT FT              T -> A (1n dBSNP:231775).  
FT FT              /FTid-VAR.013577.  
FT FT              T -> A (IN REF. 4).  
  
FT FT CONFLICT     147      147  
FT STRAND          45      47  
FT TURN            50      51  
FT STRAND          53      59  
FT STRAND          70      76  
FT STRAND          81      88  
FT STRAND          91      92  
FT TURN            99      100  
FT STRAND         104      108  
FT TURN           109      110  
FT STRAND         111      117  
FT TURN           121      123  
FT STRAND         125      132  
FT TURN           137      138  
FT STRAND         142      143  
FT STRAND         147      150  
SQ SEQUENCE        223 AA; 24656 MW; 6F9466FB2E139A5A CRC64;  
  
Query Match   100.0%; Score 653; DB 1; Length 223;  
Best Local Similarity 100.0%; Pred. No. 4.3e-60;  
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0
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OM protein - protein search, using sw model

Run on: August 23, 2003, 16:50:26 ; Search time 60 seconds

(without alignments)  
537,610 Million cell updates/sec

Title: US-09-865-321a-8\_COPY\_26\_150  
Sequence: 1 AMHVAQPAVAVLASSRGIAF.....GIGNGTQIYVIDPEPCPDS 125

Scoring table: BLOSUM62  
Gap 10.0, Gapext 0.5

Searched: 830525 segs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database:

SPTREMBL\_23:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	648	99.2	223	6	Q9BDC4 macaca mula
2	648	99.2	223	6	Q9BDN7 papio anubi
3	647	99.1	160	4	Q8TDA6
4	601	92.0	223	6	Q9BDP1
5	597	91.4	137	4	Q95653
6	592	90.7	115	4	Q9BZK2
7	573	87.7	223	6	Q9T02
8	573	87.7	223	6	Q9GKP2
9	571	87.4	223	11	Q9ULV3
10	569	87.1	223	6	Q9XSV7
11	566	86.7	223	6	Q9XTA1
12	559	85.6	223	6	Q9XST1
13	558	85.5	223	6	Q9N186
14	552	84.5	221	6	Q28090
15	540	82.7	221	6	Q97631
16	480	73.5	223	11	Q62859

17	425	65.1	174	11	Q9Z1A7	Q9Z1A7	rattus norv
18	252	38.6	68	11	Q99PF8	Q99PF8	cricketulus
19	182	27.9	102	11	Q8CH94	Q8CH94	mus musculus
20	139	21.3	173	6	Q28289	Q28289	canis faml
21	139	21.3	221	6	Q9N088	Q9N088	canis faml
22	139	21.3	221	6	Q9GKP3	Q9GKP3	canis faml
23	136	20.8	221	11	Q9ULV4	Q9ULV4	canis faml
24	130	19.9	221	6	Q02757	Q02757	felis silve
25	129.5	19.8	219	6	Q97630	Q97630	ovis silve
26	129	19.8	221	6	Q9N214	Q9N214	felis silve
27	127.5	19.5	220	6	Q9BDM6	Q9BDM6	macaca neme
28	126.5	19.4	220	6	Q9BDN5	Q9BDN5	cercocobus
29	125.5	19.2	138	6	Q8HYR3	Q8HYR3	bos taurus
30	125	19.1	220	6	Q9BDN2	Q9BDN2	callithrix
31	123.5	18.9	220	6	Q9BDN8	Q9BDN8	papio anubi
32	122.5	18.8	220	6	Q9BDM6	Q9BDM6	macaca mula
33	121	18.5	218	11	Q8CDB3	Q8CDB3	mus musculu
34	113	17.3	44	11	Q9Z1A8	Q9Z1A8	mus musculu
35	105	16.1	192	11	Q8CRD9	Q8CRD9	mus musculu
36	104	15.9	192	11	Q8CG11	Q8CG11	rattus norv
37	101	15.5	108	4	Q9UL79	Q9UL79	rattus norv
38	94.5	14.5	176	6	Q95JB8	Q95JB8	macaca fasc
39	94.5	14.5	180	6	Q8MJ02	Q8MJ02	macaca mula
40	91.5	14.0	177	4	Q14930	Q14930	homo sapien
41	91.5	14.0	201	4	Q14931	Q14931	homo sapien
42	91.5	14.0	201	4	Q14931	Q14931	homo sapien
43	90.5	13.9	235	11	Q91W12	Q91W12	mus musculu
44	89	13.6	151	6	Q8MJ01	Q8MJ01	macaca mula
45	88	13.5	152	4	Q95668	Q95668	homo sapien

## ALIGNMENTS

RESULT 1	Q9BDC4	PRELIMINARY;	PRT;	223 AA.
ID	Q9BDC4	01-JUN-2001 (TREMURel. 17, Created)		
AC	Q9BDC4	01-JUN-2001 (TREMURel. 17, Last sequence update)		
DT	01-JUN-2001 (TREMURel. 17, Last sequence update)			
DT	01-MAR-2003 (TREMURel. 23, Last annotation update)			
DE	CD152 protein precursor.			
GN	CD152			
OS	Macaca mulatta (Rhesus macaque),			
OS	Macaca nemestrina (Pig-tailed macaque), and			
OS	Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;			
OC	Cercopithecoidea; Macaca			
OX	NCBI_TaxID=9544, 9545, 9531;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	SPECIES=M.mulatta, M.nemestrina, and C.torquatus atys;			
RA	Vallinger F., Bostik P., Mayne A.E., King C.L., Genlin C.P.,			
RA	Weiss W.R., Ansari A.A.;			
RT	"Cloning, sequencing and homology analysis of nonhuman primate			
RT	Fas/Fas-Ligand and co-stimulatory molecules";			
RL	Immunogenetics 0:0-0(2001).			
DR	EMBL; AF344846; AAK37605.1; -			
DR	EMBL; AF344854; AAK37537.1; -			
DR	EMBL; AF344848; AAK37608.1; -			
DR	HSSP: P16410; IAH1			
DR	InterPro: IPR003596; Ig_V.			
DR	SMART: SM00406; IGV; I.			
KW	SIGNAL.			
FT	SIGNAL.			
FT	VARIANT			
FT	SEQUENCE			
SO	SEQUENCE			
Query Match	99.2%	Score 648;	DB 6;	Length 223;
Best Local Similarity	98.4%	Pred. No. 6,2e-61;		
Matches 123;	Conservative	2;	Mismatches	0;
		Indels	0;	Gaps
				0;

QY 1 AMHVAPAVVLASSRGIAFVCEYASPGKATEVRVTVLRQADSOQVTEVCATYMMGNELT 60  
 DB 37 AMHVAPAVVLASSRGIAFVCEYASPGKATEVRVTVLRQADSOQVTEVCATYMMGNELT 96  
 QY 61 FLDDSICTGTSSGNQVNLITQGLRAMDTGLYICKVELMPPPYLLGIGNGTQIYVIDPEP 120  
 DB 97 FLDDSICTGTSSGNQVNLITQGLRAMDTGLYICKVELMPPPYLLGIGNGTQIYVIDPEP 156  
 QY 121 CPDSD 125  
 DB 157 CPDSD 161

## RESULT 2

Q9BDN7 ID Q9BDN7 PRELIMINARY; PRT; 223 AA.

AC Q9BDN7; 01-JUN-2001 (TREMblrel. 17, Created)  
 DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)  
 DE 01-MAR-2003 (TREMblrel. 23, Last annotation update)  
 GN CD152 protein precursor.  
 OS CTIA-4.  
 OS Papio anubis (Olive baboon).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopitheciinae; Papio.  
 NC NCBL\_TaxID=9555;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21383618; PubMed=11491535;  
 RA Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,  
 RA Weiss W.R., Ansari A.A.;  
 RT "Cloning, sequencing, and homology analysis of nonhuman primate  
 RT Fas/Fas-Ligand and co-stimulatory molecules.";  
 RL Immunogenetics 53:315-328(2001).  
 DR EMBL; AF344838; AAK37534.1; -  
 DR HSSP; P16410; 1AHL.  
 DR InterPro; IPR003596; Ig\_V.  
 DR SMART; SM00406; IGV; 1.  
 KW Signal.  
 FT SIGNAL.  
 SQ SEQUENCE 223 AA; 24655 MW; EC18C279CCCC5668 CRC64;  
 Query Match 99.2%; Score 648; DB 6; Length 223;  
 Best Local Similarity 98.4%; Pred. No. 6, 2e-61;  
 Matches 123; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AMHVAPAVVLASSRGIAFVCEYASPGKATEVRVTVLRQADSOQVTEVCATYMMGNELT 60  
 DB 37 AMHVAPAVVLASSRGIAFVCEYASPGKATEVRVTVLRQADSOQVTEVCATYMMGNELT 96  
 QY 61 FLDDSICTGTSSGNQVNLITQGLRAMDTGLYICKVELMPPPYLLGIGNGTQIYVIDPEP 120  
 DB 97 FLDDSICTGTSSGNQVNLITQGLRAMDTGLYICKVELMPPPYLLGIGNGTQIYVIDPEP 156  
 QY 121 CPDSD 125  
 DB 157 CPDSD 161

## RESULT 3

Q8TDAG ID Q8TDAG PRELIMINARY; PRT; 160 AA.

AC Q8TDAG; 01-JUN-2002 (TREMblrel. 21, Created)  
 DT 01-JUN-2002 (TREMblrel. 21, Last sequence update)  
 DE 01-MAR-2003 (TREMblrel. 23, Last annotation update)  
 GN CTIA4 (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 NC NCBL\_TaxID=9606;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RA Guo J.H., Fan M.W., Bian Z., Jia R.;  
 RT "Partial sequence of CTIA4 mRNA, signal peptide and extracellular  
 RT domain";  
 RT Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF486806; AAL96664.1; -  
 DR InterPro; IPR003596; Ig\_V.  
 DR SMART; SM00406; IGV; 1.  
 FT NON\_TER 160  
 SQ SEQUENCE 160 AA; 17470 MW; 1385B4644F63836F CRC64;

## Query Match

Best Local Similarity 99.1%; Score 647; DB 4; Length 160;  
 Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMHVAPAVVLASSRGIAFVCEYASPGKATEVRVTVLRQADSOQVTEVCATYMMGNELT 60  
 DB 37 AMHVAPAVVLASSRGIAFVCEYASPGKATEVRVTVLRQADSOQVTEVCATYMMGNELT 96  
 QY 61 FLDDSICTGTSSGNQVNLITQGLRAMDTGLYICKVELMPPPYLLGIGNGTQIYVIDPEP 120  
 DB 97 FLDDSICTGTSSGNQVNLITQGLRAMDTGLYICKVELMPPPYLLGIGNGTQIYVIDPEP 156  
 QY 121 CPDSD 124  
 DB 157 CPDSD 160

## RESULT 4

Q9BDP1 ID Q9BDP1 PRELIMINARY; PRT; 223 AA.

AC Q9BDP1; 01-JUN-2001 (TREMblrel. 17, Created)  
 DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)  
 DE 01-MAR-2003 (TREMblrel. 23, Last annotation update)  
 GN CD152 protein precursor.  
 OS CTIA-4.  
 OS Actus trivirgatus (Night monkey) (Douroucouli).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Actus.  
 NC NCBL\_TaxID=9505;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21383618; PubMed=11491535;  
 RA Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,  
 RA Weiss W.R., Ansari A.A.;  
 RT "Cloning, sequencing, and homology analysis of nonhuman primate  
 RT Fas/Fas-Ligand and co-stimulatory molecules.";  
 RL Immunogenetics 53:315-328(2001).  
 DR EMBL; AF344834; AAK37530.1; -  
 DR HSSP; P16410; 1AHL.  
 DR InterPro; IPR003599; Ig.  
 DR SMART; SM00409; IGV; 1.  
 KW Signal.  
 FT SIGNAL.  
 SQ SEQUENCE 223 AA; 24813 MW; 3F702052117C1A31 CRC64;

## Query Match

Best Local Similarity 92.0%; Score 601; DB 6; Length 223;  
 Matches 113; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 AMHVAPAVVLASSRGIAFVCEYASPGKATEVRVTVLRQADSOQVTEVCATYMMGNELT 60  
 DB 37 AMHVAPAVVLASSRGIAFVCEYASPGKATEVRVTVLRQADSOQVTEVCATYMMGNELT 96  
 QY 61 FLDDSICTGTSSGNQVNLITQGLRAMDTGLYICKVELMPPPYLLGIGNGTQIYVIDPEP 120  
 DB 97 FLDDSICTGTSSGNQVNLITQGLRAMDTGLYICKVELMPPPYLLGIGNGTQIYVIDPEP 156  
 QY 121 CPDSD 125  
 DB 157 CPDSD 161

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 23, 2003, 16:43:01 ; Search time 60.5 Seconds

(without alignments)  
327.947 Million cell updates/sec

Title: US-09-865-321a-8\_COPY\_26\_150

Perfect score: 653  
Sequence: 1 AMHVAQPAVVLASSRGIA SF.....GIGNGTQIYVIDPEPCDSD 125

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT.\*  
2: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT.\*  
3: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT.\*  
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21: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT.\*  
22: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT.\*  
23: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT.\*  
24: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysts of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	653	100.0	187	20	AAV41130
2	653	100.0	187	20	AAW97615
3	653	100.0	187	20	AAW97610
4	653	100.0	211	20	AAW87560
5	653	100.0	212	14	AAW81040
6	653	100.0	212	15	AAW80134
7	653	100.0	212	16	AAW77642
8	653	100.0	212	20	AAW43479
9	653	100.0	212	20	AAW81584

10	653	100.0	212	23	ABW78106
11	653	100.0	212	23	AAU75124
12	653	100.0	212	24	ABP56715
13	653	100.0	223	21	AAV15129
14	653	100.0	223	23	AAU74508
15	653	100.0	223	23	AAU74509
16	653	100.0	364	21	AAV93698
17	653	100.0	374	18	AAW26206
18	653	100.0	374	18	AAW26207
19	653	100.0	377	18	AAW26208
20	653	100.0	383	23	ABW78107
21	653	100.0	383	23	AAW50556
22	653	100.0	383	23	AAU75125
23	653	100.0	383	23	AAW47861
24	653	100.0	383	24	ABP56716
25	653	100.0	383	24	ABP56722
26	653	100.0	502	24	ABJ37107
27	650	99.5	187	17	AAW86945
28	649	99.4	212	23	AAU75133
29	648	99.2	212	23	AAU75126
30	648	99.2	223	22	AAW65519
31	648	99.2	223	23	ABG32819
32	648	99.2	223	23	AAE13270
33	647	99.1	168	19	AAW42340
34	647	99.1	212	18	AAU75132
35	647	99.1	223	18	AAW25111
36	647	99.1	223	22	AAU00687
37	647	99.1	223	23	ABW79934
38	647	99.1	357	19	AAW68134
39	647	99.1	377	19	ABJ37105
40	647	99.1	470	19	AAW68135
41	646	98.9	212	23	AAU75131
42	646	98.9	383	23	ABW78101
43	646	98.9	383	23	AAW50655
44	646	98.9	383	23	AAU75119
45	646	98.9	383	24	ABP56718

#### ALIGNMENTS

AAV41130	standard; Protein: 187 AA.
AAV41130	
24-JAN-2000	(first entry)
CTLA4	receptor with oncostatin M signal peptide.
DE	Monoclonal antibody; Mab; extracellular domain; CTLA4; B7 antigen;
KW	T cell interaction; inflammation; autoimmunity; transplantation; GCHD;
KW	neoplasia; infectious disease; graft versus host disease; psoriasis;
KW	immune disorder; lymphoma; leukemia; autoimmune disease; arthritis;
KW	diabetes mellitus; oncostatin M; CD28 protein;
OS	Homo sapiens.
PN	US5977318-A.
XX	02-NOV-1999.
PD	
XX	07-JUN-1995;
PF	95US-0488062.
XX	18-JAN-1995;
PR	95US-0375390.
PR	27-JUN-1991;
PR	91US-0723617.
PR	22-JAN-1993;
PR	93US-0008898.
XX	15-APR-1994;
XX	94US-0228208.
PA	(BRIM ) BRISTOL-MYERS SQUIBB CO.
XX	Kleiner PA, Brady W, Damle NK, Linsley PS, Ledbetter JA;



QY 1 AMHVAOPAVYVLASSRGIAISFVCEYASPGKATEVRVTVLRQADSQVTEVCATYMMGNELT 60  
 DB 37 AMHVAOPAVYVLASSRGIAISFVCEYASPGKATEVRVTVLRQADSQVTEVCATYMMGNELT 96  
 QY 61 FLDDSICTGTSSGNQVNLITIGLRAMDGTGLYICKVELMPPPYLYGIGNGTQIYVIDPEP 120  
 DB 97 FLDDSICTGTSSGNQVNLITIGLRAMDGTGLYICKVELMPPPYLYGIGNGTQIYVIDPEP 156  
 QY 121 CPDSD 125  
 DB 157 CPDSD 161

## RESULT 2

09BDN7 PRELIMINARY: PRT: 223 AA.

AC 09BDN7 01-JUN-2001 (TREMBLrel. 17, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
 DE CD152 protein precursor.  
 GN CTLA-4  
 OS Papio anubis (Olive baboon).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecinae; Papio.  
 OX NCBI\_TaxID=9555;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-21383618; PubMed-11491535;  
 RA Villinger F., Boslik P., Mayne A.E., King C.L., Genain C.P.,  
 RA Weiss W.R., Ansari A.A.;  
 RT "Cloning, sequencing, and homology analysis of nonhuman primate  
 Fas/Fas-ligand and co-stimulatory molecules.";  
 RL Immunogenetics 53:335-328(2001).  
 DR EMBL; AF344838; AAK37534.1;  
 DR HSSP; P16410; IAH1.  
 DR InterPro; IPR003596; I9-V.  
 DR SMART; SM00406; IGV; 1.  
 KW Signal.  
 FT SIGNAL.  
 SQ SEQUENCE 223 AA; 24655 MW; EC18C279CCCC5668 CRC64;

Query Match 99.2%; Score 648; DB 6; Length 223;  
 Best Local Similarity 98.4%; Pred. No. 6.2e-61;  
 Matches 123; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

1 AMHVAOPAVYVLASSRGIAISFVCEYASPGKATEVRVTVLRQADSQVTEVCATYMMGNELT 60  
 DB 37 AMHVAOPAVYVLASSRGIAISFVCEYASPGKATEVRVTVLRQADSQVTEVCATYMMGNELT 96  
 QY 61 FLDDSICTGTSSGNQVNLITIGLRAMDGTGLYICKVELMPPPYLYGIGNGTQIYVIDPEP 120  
 DB 97 FLDDSICTGTSSGNQVNLITIGLRAMDGTGLYICKVELMPPPYLYGIGNGTQIYVIDPEP 156

T; 160 AA.

ed)  
 sequence update)  
 notation update)

ta; Vertebrata; Euteleostomi;  
 hml; Homidae; Homo.

RP SEQUENCE FROM N.A.  
 RA Guo J.H., Fan M.W., Bian Z., Jia R.;  
 RT "Partial sequence of CTLA4 mRNA, signal peptide and extracellular  
 RT domain.";  
 RL Submitted (EBB-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF486806; AAL96664.1;  
 DR InterPro; IPR003596; I9-V.  
 DR SMART; SM00406; IGV; 1.  
 FT NON-TER  
 SQ SEQUENCE 160 AA; 17470 MW; 1385B4644F6386F CRC64;

Query Match 99.1%; Score 647; DB 4; Length 160;  
 Best Local Similarity 100.0%; Pred. No. 5.2e-61;  
 Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMHVAOPAVYVLASSRGIAISFVCEYASPGKATEVRVTVLRQADSQVTEVCATYMMGNELT 60  
 DB 37 AMHVAOPAVYVLASSRGIAISFVCEYASPGKATEVRVTVLRQADSQVTEVCATYMMGNELT 96  
 QY 61 FLDDSICTGTSSGNQVNLITIGLRAMDGTGLYICKVELMPPPYLYGIGNGTQIYVIDPEP 120  
 DB 97 FLDDSICTGTSSGNQVNLITIGLRAMDGTGLYICKVELMPPPYLYGIGNGTQIYVIDPEP 156  
 QY 121 CPDSD 124  
 DB 157 CPDSD 160

## RESULT 4

09BDP1 PRELIMINARY: PRT: 223 AA.

AC 09BDP1 01-JUN-2001 (TREMBLrel. 17, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
 DE CD152 protein precursor.  
 GN CTLA-4  
 OS Aotus trivirgatus (Night monkey) (Douroucoulli).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.  
 OX NCBI\_TaxID=9505;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-21383618; PubMed-11491535;  
 RA Villinger F., Boslik P., Mayne A.E., King C.L., Genain C.P.,  
 RA Weiss W.R., Ansari A.A.;  
 RT "Cloning, sequencing, and homology analysis of nonhuman primate  
 Fas/Fas-ligand and co-stimulatory molecules.";  
 RL Immunogenetics 53:335-328(2001).  
 DR EMBL; AF344834; AAK37530.1;  
 DR HSSP; P16410; IAH1.  
 DR InterPro; IPR003599; I9.  
 DR SMART; SM00409; IGV; 1.  
 KW Signal.  
 FT SIGNAL.  
 SQ SEQUENCE 223 AA; 24813 MW; 3F702052117C1431 CRC64;

Query Match 92.0%; Score 601; DB 6; Length 223;  
 Best Local Similarity 90.4%; Pred. No. 6.3e-56;  
 Matches 113; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 AMHVAOPAVYVLASSRGIAISFVCEYASPGKATEVRVTVLRQADSQVTEVCATYMMGNELT 60  
 DB 37 AMHVAOPAVYVLASSRGIAISFVCEYASPGKATEVRVTVLRQADSQVTEVCATYMMGNELT 96  
 QY 61 FLDDSICTGTSSGNQVNLITIGLRAMDGTGLYICKVELMPPPYLYGIGNGTQIYVIDPEP 120  
 DB 97 FLDDSICTGTSSGNQVNLITIGLRAMDGTGLYICKVELMPPPYLYGIGNGTQIYVIDPEP 156  
 QY 121 CPDSD 125  
 DB 157 CPDSD 161

ersion 5.1.6  
2003 CompuGen Ltd.

w model

: 50.26 ; Search time 60 Seconds  
(without alignments)  
537.610 Million cell updates/sec

3\_COPY\_26\_150

3SKGIAF.....GIGNCTOIVIDPECPDSD 125

0.0 ; Gapext 0.5

25 seqs, 258052604 residues

of hits satisfying chosen parameters: 830525

um DB seq length: 0  
Maximum Match 0%

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Listing first 45 summaries

SPTREMBL\_23:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_protist:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	648	99.2	223	6 O9BDC4	O9BDC4 macaca mla
2	648	99.2	223	6 O9BDN7	O9BDN7 papio anubi
3	647	99.1	160	4 O8TDA6	O8TDA6 homo sapien
4	601	92.0	223	6 O9BDP1	O9BDP1 actus trivi
5	597	91.4	137	4 O9S6S3	O9S6S3 homo sapien
6	592	90.7	115	4 O9BZK2	O9BZK2 homo sapien
7	573	87.7	223	6 O9RT02	O9RT02 canis famli
8	573	87.7	223	6 O9GKP2	O9GKP2 canis famli
9	571	87.4	223	11 O9JLV3	O9JLV3 marmota mon
10	569	87.1	223	6 O9XSY7	O9XSY7 felis silve
11	566	86.7	223	6 O9XTA1	O9XTA1 felis silve
12	559	85.6	223	6 O9XSI1	O9XSI1 canis famli
13	558	85.5	223	6 O9N186	O9N186 sus scrofa
14	552	84.5	221	6 O28090	O28090 bos taurus
15	540	82.7	221	6 O97631	O97631 ovis aries
16	480	73.5	223	11 O62859	O62859 ratius norv

17	425	65.1	174	11 O9Z1A7	O9Z1A7 ratius norv
18	252	38.6	68	11 O99PF8	O99PF8 cricetus
19	182	27.9	102	11 O8CH94	O8CH94 mus musculu
20	139	21.3	173	6 O28289	O28289 canis famli
21	139	21.3	221	6 O9N0N8	O9N0N8 canis famli
22	139	21.3	221	6 O9GKP3	O9GKP3 canis famli
23	136	20.8	221	11 O9JLV4	O9JLV4 marmota mon
24	130	19.9	221	6 O02757	O02757 felis silve
25	129.5	19.8	219	6 O97630	O97630 ovis aries
26	129	19.8	221	6 O9N214	O9N214 felis silve
27	127.5	19.5	220	6 O9BDM8	O9BDM8 macaca neme
28	126.5	19.4	220	6 O9BDN5	O9BDN5 cercocobus
29	125.5	19.2	138	6 O8HTR9	O8HTR9 bos taurus
30	125	19.1	220	6 O9BDN2	O9BDN2 callithrix
31	123.5	18.9	220	6 O9BDN8	O9BDN8 papio anubi
32	122.5	18.8	220	6 O9BDM6	O9BDM6 macaca mla
33	121	18.5	218	11 O8CDB3	O8CDB3 mus musculu
34	113	17.3	44	11 O9Z1A8	O9Z1A8 mus musculu
35	105	16.1	192	11 O8CFD9	O8CFD9 ratius norv
36	104	15.9	192	11 O8CG11	O8CG11 ratius norv
37	101	15.5	108	4 O9UL79	O9UL79 homo sapien
38	94.5	14.5	176	6 O95JH8	O95JH8 macaca fasc
39	94.5	14.5	180	6 O8MJ02	O8MJ02 macaca mla
40	91.5	14.0	177	4 O14930	O14930 homo sapien
41	91.5	14.0	190	4 O14932	O14932 homo sapien
42	91.5	14.0	201	4 O14931	O14931 homo sapien
43	90.5	13.9	235	11 O91W12	O91W12 mus musculu
44	89	13.6	151	6 O8MJ01	O8MJ01 macaca mla
45	88	13.5	152	4 O95668	O95668 homo sapien

## ALIGNMENTS

RESULT 1  
ID O9BDC4 PRELIMINARY: PRT: 223 AA.

AC O9BDC4:

DT 01-JUN-2001 (TREMBLrel. 17, Created)

DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)

DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)

DE CD152 protein precursor.

GN CTR4-4.

OS Macaca mulatta (Rhesus macaque),

OS Macaca nemestrina (Pig-tailed macaque), and

OS Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;

OC Cercopithecinae; Macaca.

OX NCBI\_TaxID=9544, 9545, 9531;

RN [1]

RP SEQUENCE FROM N.A.

RC SPECIES=M.mulatta, M.nemestrina, and C.torquatus atys;

RA Villinger F., Bostik P., Wayne A.E., King C.L., Genain C.P.,

RA Weiss W.R., Ansari A.A.;

RT "Cloning, sequencing and homology analysis of nonhuman primate

RT Fas/Fas-ligand and co-stimulatory molecules.";

RL Immunogenetics 0:0-0(2001);

RL EMBL; AF344846; AAK37805.1;

DR EMBL; AF344854; AAK37537.1;

DR EMBL; AF344848; AAK37608.1;

DR HSSP; P16410; IAH1.

DR Interpro: IPR003596; IG-V.

DR SMART: SM00406; IGV; 1.

KW SIGNAL.

FT SIGNAL.

FT VARIANT.

SO SEQUENCE

POTENTIAL.

N -> D.

BDE42248A0398FA CRC64;

24683 MM;

99.2%;

Score 648;

DB 6;

Length 223;

Best Local Similarity 98.4%;

Pred. No. 6,2e-61;

Matches 123; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: August 23, 2003, 16:57:06 ; Search time 36 Seconds

(without alignments)  
458,200 Million cell updates/sec

Title: US-09-865-321a-8\_copy\_26\_150

Perfect score: 653  
Sequence: 1 AMHVAQPAVVLASSRGIAASF.....GICNGTQIYIDPECPDSD 125

## Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 497079 seqs, 131961718 residues

Total number of hits satisfying chosen parameters: 497079

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

## Database :

Published\_Applications\_AA:\*  
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2: /cgn2\_6/ptodata/1/pubppaa/PCT\_NEW\_PUB.pep:\*  
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4: /cgn2\_6/ptodata/1/pubppaa/US06\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/1/pubppaa/US07\_NEW\_PUB.pep:\*  
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7: /cgn2\_6/ptodata/1/pubppaa/US08\_NEW\_PUB.pep:\*  
8: /cgn2\_6/ptodata/1/pubppaa/US08\_PUBCOMB.pep:\*  
9: /cgn2\_6/ptodata/1/pubppaa/US09A\_PUBCOMB.pep:\*  
10: /cgn2\_6/ptodata/1/pubppaa/US09B\_PUBCOMB.pep:\*  
11: /cgn2\_6/ptodata/1/pubppaa/US09C\_PUBCOMB.pep:\*  
12: /cgn2\_6/ptodata/1/pubppaa/US09\_NEW\_PUB.pep:\*  
13: /cgn2\_6/ptodata/1/pubppaa/US10A\_PUBCOMB.pep:\*  
14: /cgn2\_6/ptodata/1/pubppaa/US10B\_PUBCOMB.pep:\*  
15: /cgn2\_6/ptodata/1/pubppaa/US10C\_PUBCOMB.pep:\*  
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18: /cgn2\_6/ptodata/1/pubppaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	653	100.0	151	US-10-207-655-309	Sequence 309, App
2	653	100.0	212	US-09-898-195A-17	Sequence 17, App1
3	653	100.0	212	US-10-057-288-12	Sequence 12, App1
4	653	100.0	212	US-10-155-514-2	Sequence 2, App1
5	653	100.0	374	US-10-027-075-26	Sequence 26, App1
6	653	100.0	374	US-10-027-075-24	Sequence 24, App1
7	653	100.0	377	US-10-027-075-24	Sequence 24, App1
8	653	100.0	382	US-10-207-655-307	Sequence 307, App
9	653	100.0	382	US-10-207-655-316	Sequence 316, App
10	653	100.0	383	US-09-865-321-8	Sequence 8, App1
11	653	100.0	383	US-09-898-195A-19	Sequence 19, App1
12	653	100.0	383	US-10-057-288-14	Sequence 14, App1
13	653	100.0	383	US-10-155-514-4	Sequence 4, App1
14	653	100.0	383	US-10-155-514-16	Sequence 16, App1
15	653	100.0	399	US-10-207-655-320	Sequence 320, App

16	653	100.0	403	15	US-10-207-655-318	Sequence 318, App
17	648	99.2	223	11	US-09-835-297-2	Sequence 2, App1
18	648	99.2	223	15	US-10-211-207-3	Sequence 3, App1
19	647	99.1	168	10	US-09-845-899A-7	Sequence 7, App1
20	647	99.1	223	10	US-09-989-545-21	Sequence 21, App1
21	647	99.1	223	15	US-10-225-519-8	Sequence 8, App1
22	647	99.1	223	15	US-10-207-655-101	Sequence 101, App
23	646	98.9	383	10	US-09-865-321-6	Sequence 6, App1
24	646	98.9	383	15	US-09-898-195A-7	Sequence 7, App1
25	646	98.9	383	15	US-10-057-288-2	Sequence 2, App1
26	646	98.9	383	15	US-10-155-514-8	Sequence 8, App1
27	643	98.5	260	15	US-10-225-519-4	Sequence 4, App1
28	642	98.3	383	11	US-09-898-195A-13	Sequence 13, App1
29	642	98.3	383	15	US-10-057-288-8	Sequence 8, App1
30	642	98.3	383	15	US-10-155-514-12	Sequence 12, App1
31	641	98.2	124	15	US-10-207-655-314	Sequence 314, App
32	641	98.2	383	11	US-09-898-195A-11	Sequence 11, App1
33	641	98.2	383	15	US-10-057-288-6	Sequence 6, App1
34	641	98.2	383	15	US-10-155-514-10	Sequence 10, App1
35	640	98.0	187	11	US-09-014-761-1	Sequence 1, App1
36	640	98.0	223	14	US-10-107-828-26	Sequence 26, App1
37	640	98.0	223	14	US-10-107-807-26	Sequence 26, App1
38	640	98.0	223	14	US-10-107-868-26	Sequence 26, App1
39	640	98.0	223	15	US-10-301-056-26	Sequence 26, App1
40	640	98.0	383	10	US-09-865-321-4	Sequence 4, App1
41	640	98.0	383	11	US-09-898-195A-9	Sequence 9, App1
42	640	98.0	383	15	US-10-057-288-4	Sequence 4, App1
43	640	98.0	383	15	US-10-155-514-6	Sequence 6, App1
44	639	97.9	383	11	US-09-898-195A-15	Sequence 15, App1
45	639	97.9	383	15	US-10-057-288-10	Sequence 10, App1

## ALIGNMENTS

RESULT 1  
US-10-207-655-309  
Sequence 309, Application US/10207655  
Publication No. US20030118592A1  
GENERAL INFORMATION:  
APPLICANT: Ledbetter, Jeffrey A.  
TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS  
FILE REFERENCE: 390069.401C1  
CURRENT APPLICATION NUMBER: US/10/207,655  
CURRENT FILING DATE: 2002-07-25  
NUMBER OF SEQ ID NOS: 426  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 309  
LENGTH: 151  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: fusion polypeptide  
US-10-207-655-309

Query Match 100.0%; Score 653; DB 15; Length 151;  
Best Local Similarity 100.0%; Pred. No. 1.4e-62;  
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AMHVAQPAVVLASSRGIAFVCEYASFGKATEVRVTLROADSQVTEVCATYMGNELT 60  
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Db 26 AMHVAQPAVVLASSRGIAFVCEYASFGKATEVRVTLROADSQVTEVCATYMGNELT 85  
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QY 61 FLDDISCTGSSGNQVLTLOGLRAMDTGLYICKVELMPPPYLLGIGNGTQIYIDPEP 120  
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Db 86 FLDDISCTGSSGNQVLTLOGLRAMDTGLYICKVELMPPPYLLGIGNGTQIYIDPEP 145  
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QY 121 CPDSD 125  
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Db 146 CPDSD 150

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RESULT 2
US-09-898-195A-17
; Sequence 17, Application US/09898195A
; Publication No. US20030083246A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Robert
; APPLICANT: Carr, Suzette
; APPLICANT: Hagerly, David
; APPLICANT: Peach, Robert J
; APPLICANT: Becker, Jean-Claude
; TITLE OF INVENTION: METHODS FOR TREATING RHEUMATIC DISEASES USING A SOLUBLE
; FILE REFERENCE: D0030NF/30436.55USU1
; CURRENT APPLICATION NUMBER: US/09/898,195A
; PRIOR FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: 60/215,913
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-898-195A-17

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Best Local Similarity 100.0%; Pred. No. 2.1e-62;
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    |||||||

QY 61 FLDDISCTGTSSGNOVNLTIGLRAMDGLYICKVELMPPPPYLGINGTQIYVIDEP 120
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DB 86 FLDDISCTGTSSGNOVNLTIGLRAMDGLYICKVELMPPPPYLGINGTQIYVIDEP 145
    |||||||

QY 121 CPDSD 125
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DB 146 CPDSD 150

RESULT 3
US-10-057-288-12
; Sequence 12, Application US/10057288
; Publication No. US20030007968A1
; GENERAL INFORMATION:
; APPLICANT: Larsen, Christian P.
; APPLICANT: Pearson, Thomas C.
; APPLICANT: Waller, Edmund K.
; APPLICANT: Adams, Andrew B.
; TITLE OF INVENTION: METHODS OF INDUCING ORGAN TRANSPLANT TOLERANCE AND
; FILE REFERENCE: D0136NP/30436.580SU1
; CURRENT APPLICATION NUMBER: US/10/057,288
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: 60/264,528
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/303,142
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-057-288-12

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Best Local Similarity 100.0%; Pred. No. 2.1e-62;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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    |||||||
DB 26 AMHVAQPAVVLASSRGISAFVCEYASPGKATEVRVTVLRQADSOYTEVCATYMMGNELT 85
    |||||||

QY 61 FLDDISCTGTSSGNOVNLTIGLRAMDGLYICKVELMPPPPYLGINGTQIYVIDEP 120
    |||||||
DB 86 FLDDISCTGTSSGNOVNLTIGLRAMDGLYICKVELMPPPPYLGINGTQIYVIDEP 145
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QY 121 CPDSD 125
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DB 146 CPDSD 150
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DB 26 AMHVAQPAVVLASSRGISAFVCEYASPGKATEVRVTVLRQADSOYTEVCATYMMGNELT 85
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QY 61 FLDDISCTGTSSGNOVNLTIGLRAMDGLYICKVELMPPPPYLGINGTQIYVIDEP 120
    |||||||
DB 86 FLDDISCTGTSSGNOVNLTIGLRAMDGLYICKVELMPPPPYLGINGTQIYVIDEP 145
    |||||||

QY 121 CPDSD 125
    |||||
DB 146 CPDSD 150

RESULT 4
US-10-155-514-2
; Sequence 2, Application US/10155514
; Publication No. US20030022836A1
; GENERAL INFORMATION:
; APPLICANT: Larsen, Christian P.
; APPLICANT: Pearson, Thomas C.
; APPLICANT: Adams, Andrew B.
; TITLE OF INVENTION: METHODS FOR PROTECTING ALLOGENEIC ISLET TRANSPLANT USING SOLUB
; FILE REFERENCE: D0173NP / 30436.620SU1
; CURRENT APPLICATION NUMBER: US/10/155,514
; PRIOR FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: 60/293,402
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-155-514-2

Query Match          100.0%; Score 653; DB 15; Length 212;
Best Local Similarity 100.0%; Pred. No. 2.1e-62;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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    |||||||
DB 26 AMHVAQPAVVLASSRGISAFVCEYASPGKATEVRVTVLRQADSOYTEVCATYMMGNELT 85
    |||||||

QY 61 FLDDISCTGTSSGNOVNLTIGLRAMDGLYICKVELMPPPPYLGINGTQIYVIDEP 120
    |||||||
DB 86 FLDDISCTGTSSGNOVNLTIGLRAMDGLYICKVELMPPPPYLGINGTQIYVIDEP 145
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QY 121 CPDSD 125
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DB 146 CPDSD 150

RESULT 5
US-10-027-075-26
; Sequence 26, Application US/10027075
; Publication No. US20020114814A1
; GENERAL INFORMATION:
; APPLICANT: Gray, Gary S. et al.
; TITLE OF INVENTION: CTLA4-Immunoglobulin Fusion Proteins
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 23, 2003, 16:52:21 ; Search time 20.5 Seconds  
(without alignments)  
257.993 Million cell updates/sec

Title: US-09-865-321a-8\_COPY\_26\_150

Perfect score: 653  
Sequence: 1 AMHYAOPAVYVLAASSRGIAASF.....GIGNGTQIYIDPECPDSD 125

Scoring table:  
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Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310658 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	653	100.0	187	1	US-08-067-684-14 Sequence 14, Appl
2	653	100.0	187	1	US-08-008-898-14 Sequence 14, Appl
3	653	100.0	187	2	US-08-459-818-14 Sequence 14, Appl
4	653	100.0	187	2	US-08-889-666-14 Sequence 14, Appl
5	653	100.0	187	2	US-08-455-078-14 Sequence 14, Appl
6	653	100.0	187	2	US-08-725-776-14 Sequence 14, Appl
7	653	100.0	187	2	US-08-488-062-14 Sequence 14, Appl
8	653	100.0	187	3	US-08-228-208A-14 Sequence 14, Appl
9	653	100.0	223	4	US-08-228-208A-17 Sequence 17, Appl
10	653	100.0	374	4	US-08-227-595-26 Sequence 26, Appl
11	653	100.0	374	4	US-08-227-595-26 Sequence 26, Appl
12	653	100.0	374	4	US-08-227-595-26 Sequence 26, Appl
13	650	99.5	187	5	US-09-227-595-24 Sequence 24, Appl
14	644	98.6	124	3	US-08-630-172-4 Sequence 4, Appl
15	644	98.6	124	3	US-08-630-172-4 Sequence 4, Appl
16	644	98.6	124	3	US-08-630-172-4 Sequence 4, Appl
17	644	98.6	357	3	US-08-630-172-20 Sequence 20, Appl
18	630.5	96.6	253	2	US-09-375-419-20 Sequence 20, Appl
19	630.5	96.6	253	2	US-08-459-818-20 Sequence 20, Appl
20	630.5	96.6	253	2	US-08-889-666-20 Sequence 20, Appl
21	630.5	96.6	253	2	US-08-465-078-20 Sequence 20, Appl
22	630.5	96.6	253	2	US-08-725-776-20 Sequence 20, Appl
23	630.5	96.6	502	2	US-08-459-818-19 Sequence 19, Appl
24	630.5	96.6	502	2	US-08-889-666-19 Sequence 19, Appl
25	630.5	96.6	502	2	US-08-465-078-19 Sequence 19, Appl
26	630.5	96.6	502	2	US-08-725-776-19 Sequence 19, Appl
27	630.5	96.6	502	2	US-08-488-062-19 Sequence 19, Appl

28	613	93.9	234	1	US-08-505-058-1 Sequence 1, Appl
29	613	93.9	234	2	US-08-459-818-21 Sequence 21, Appl
30	613	93.9	234	2	US-08-889-666-21 Sequence 21, Appl
31	613	93.9	234	2	US-08-465-078-21 Sequence 21, Appl
32	613	93.9	234	2	US-08-725-776-21 Sequence 21, Appl
33	613	93.9	234	2	US-08-488-062-21 Sequence 21, Appl
34	597	91.4	137	3	US-08-804-180C-2 Sequence 30, Appl
35	583	89.3	238	4	US-09-227-595-30 Sequence 30, Appl
36	583	89.3	238	4	US-09-227-595-30 Sequence 30, Appl
37	563	86.2	109	4	US-09-460-384-34 Sequence 34, Appl
38	547	83.8	223	4	US-09-303-040-10 Sequence 32, Appl
39	439	67.2	223	3	US-08-228-208A-18 Sequence 18, Appl
40	425	65.1	174	3	US-08-804-180C-4 Sequence 10, Appl
41	408	62.5	234	1	US-08-505-058-2 Sequence 4, Appl
42	408	62.5	234	2	US-08-459-818-22 Sequence 2, Appl
43	408	62.5	234	2	US-08-889-666-22 Sequence 22, Appl
44	408	62.5	234	2	US-08-465-078-22 Sequence 22, Appl
45	408	62.5	234	2	US-08-725-776-22 Sequence 22, Appl

#### ALIGNMENTS

RESULT 1  
US-08-067-684-14  
Sequence 14, Application US/08067684  
Patent No. 5434131  
GENERAL INFORMATION:  
APPLICANT: Linsley, Peter S.  
APPLICANT: Ledbetter, Jeffrey A.  
APPLICANT: Damle, Nitin K.  
APPLICANT: Brady, William  
TITLE OF INVENTION: CTLA4 RECEPTOR AND METHODS FOR ITS USE  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sheldon & Mak  
STREET: 225 South Lake Avenue, Suite 900  
CITY: Pasadena  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 91101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/067,684  
FILING DATE: 26-MAY-1993  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Adriano, Sarah B.  
REGISTRATION NUMBER: 34,470  
REFERENCE/DOCKET NUMBER: 7848-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 310/479-8340  
TELEFAX: 310/312-9900  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 187 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHEICAL: NO  
ANTI-SENSE: NO  
US-08-067-684-14  
Query Match 100.0%; Score 653; DB 1; Length 187;  
Best Local Similarity 100.0%; Pred. No. 2.4e-63;  
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1 AMHYAOPAVYVLAASSRGIAASFVCHVYASPGKATEVTVTLROADSQVTEVCATYMMGNELT 60  
|||||

Db 1 AMHVAOPAVVLASSRGIAFVCEYASPGKATEVRVTVLRQADSOVTEVCATYMGNELT 60  
QY 61 FLDDSGTGTSSGNQVNLTIQGLRAMDTGLYICKVELMPPPYIIGNGTOIYVIDEP 120  
Db 61 FLDDSGTGTSSGNQVNLTIQGLRAMDTGLYICKVELMPPPYIIGNGTOIYVIDEP 120  
QY 121 CPDSD 125  
Db 121 CPDSD 125

## RESULT 2

US-08-008-898-14

; Sequence 14, Application US/08008898  
; Patent No. 5770197  
; GENERAL INFORMATION:  
; APPLICANT: Linsley, Peter S  
; APPLICANT: Ledbetter, Jeffrey A  
; APPLICANT: Damle, Nitin K  
; APPLICANT: Brady, William  
; TITLE OF INVENTION: CTLA4 RECEPTOR AND METHODS FOR ITS USE  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sheldon & Max  
; STREET: 201 South Lake Avenue, Suite 800  
; CITY: Pasadena  
; STATE: California  
; COUNTRY: United States  
; ZIP: 91101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/008.898  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/723.617  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mandel, Saralynn  
; REGISTRATION NUMBER: 31,853  
; REFERENCE/DOCKET NUMBER: 7848  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (818) 796-4000  
; TELEFAX: (818) 795-6321  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 187 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-008-898-14

Query Match 100.0%; Score 653; DB 1; Length 187;  
Best Local Similarity 100.0%; Pred. No. 2.4e-63;  
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMHVAOPAVVLASSRGIAFVCEYASPGKATEVRVTVLRQADSOVTEVCATYMGNELT 60  
Db 1 AMHVAOPAVVLASSRGIAFVCEYASPGKATEVRVTVLRQADSOVTEVCATYMGNELT 60  
QY 61 FLDDSGTGTSSGNQVNLTIQGLRAMDTGLYICKVELMPPPYIIGNGTOIYVIDEP 120  
Db 61 FLDDSGTGTSSGNQVNLTIQGLRAMDTGLYICKVELMPPPYIIGNGTOIYVIDEP 120  
QY 121 CPDSD 125  
Db 121 CPDSD 125

## RESULT 3

US-08-459-818-14

; Sequence 14, Application US/08459818  
; Patent No. 5851795  
; GENERAL INFORMATION:  
; APPLICANT: Linsley, Peter S.  
; APPLICANT: Ledbetter, Jeffrey A.  
; APPLICANT: Damle, Nitin K.  
; APPLICANT: Brady, William  
; TITLE OF INVENTION: CTLA4 Receptor and Uses Thereof  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merchant & Gould  
; STREET: 11150 Santa Monica Blvd., Suite 400  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: USA  
; ZIP: 90025  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: FastSeq 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/459.818  
; FILING DATE: 02-JUN-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Adriano, Sarah B.  
; REGISTRATION NUMBER: 34,470  
; REFERENCE/DOCKET NUMBER: 30436.35US02  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 310-445-1140  
; TELEFAX: 310-445-9031  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 187 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-459-818-14

Query Match 100.0%; Score 653; DB 2; Length 187;  
Best Local Similarity 100.0%; Pred. No. 2.4e-63;  
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMHVAOPAVVLASSRGIAFVCEYASPGKATEVRVTVLRQADSOVTEVCATYMGNELT 60  
Db 1 AMHVAOPAVVLASSRGIAFVCEYASPGKATEVRVTVLRQADSOVTEVCATYMGNELT 60  
QY 61 FLDDSGTGTSSGNQVNLTIQGLRAMDTGLYICKVELMPPPYIIGNGTOIYVIDEP 120  
Db 61 FLDDSGTGTSSGNQVNLTIQGLRAMDTGLYICKVELMPPPYIIGNGTOIYVIDEP 120  
QY 121 CPDSD 125  
Db 121 CPDSD 125

## RESULT 4

US-08-889-666-14

; Sequence 14, Application US/08889666  
; Patent No. 5885579  
; GENERAL INFORMATION:  
; APPLICANT: Linsley, Peter S.  
; APPLICANT: Ledbetter, Jeffrey A.  
; APPLICANT: Damle, Nitin K.  
; APPLICANT: Brady, William  
; APPLICANT: Kienert, Peter A.  
; TITLE OF INVENTION: CTLA4 Receptor and Uses Thereof  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merchant & Gould